

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2001, 09:51:08 ; Search time 2146.18 Seconds
(without alignments)
12830.314 Million cell updates/sec

Title: US-09-297-703A-28
Perfect score: 2913
Sequence: 1 ctcttaactctcagcga.....aaaaacacacacacacacatccatg 2913

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 segs, 4726426750 residues
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

Result	Query
No.	Score Match Length DB ID

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4	412.6	14.2	825	144 BF065047
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6	400.2	13.7	650	167 BE427534
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9	383.8	13.2	639	111 AM065029
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22	271	9.3	834	13 AA880470
23	270.2	9.3	508	152 BE366689
24	270	9.3	501	159 NE5726
25	266.2	9.1	447	115 AW397653
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41	238.6	8.0	454	158 H36370
42	233.2	8.0	375	167 BE149358
43	228.4	7.8	326	136 BE520887
44	227.8	7.8	548	113 AM258093
45	226.8	7.8	375	175 BG240463

Methods Enzymol. 303, 19-44 (1999)

2 (sites)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

3 (sites)
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M., Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiyake, S., Inoue, K., Togawa, Y., Izawa, M., Matsutani, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Watanabe, K., Okazaki, Y., Muramatsu, M., Inoue, Y., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

4 (sites)
The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection. *Nature* 409, 685-690 (2001)

5 (bases 1 to 2738)
Akechi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagata, K., Ishii, Y., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hori, F., Imotani, K., Inari, Y., Itoh, M., Izawa, M., Kato, H., Kawaji, S., Kojima, Y., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shigaoka, A., Shiraki, T., Sugabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

Direct Submission
Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to

Source

SOURCE
mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
clone_11b:RIKEN full-length enriched mouse cDNA library
Clone:2310045H19.

ORGANISM
mus musculus

REFERENCE
Eukaryotic; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
1 (sities)

AUTHORS
Carninci,P. and Hayashizaki,Y.

TITLE
High-efficiency full-length cDNA cloning

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ORIGIN

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Matches 1166; Conservative 0; Mismatches 825; Indels 48; Gaps 5;

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 SOURCE barley.
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 REFERENCE 1 (bases 1 to 731)
 AUTHORS Wing,R., Close,T.J., Kleinof,A., Wise,R., Begum,D., Frisch,D., Yu
 ,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
 ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
 Wood,T.
 TITLE Development of a genetically and physically anchored EST resource
 for barley genomics
 JOURNAL Unpublished (2000)
 COMMENT On Aug 21, 2000 this sequence version replaced gi:9860088.
 CONTACT: Wing RA
 CLEMSON UNIVERSITY Genomics Institute
 CLEMSON UNIVERSITY
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: AATTACCCCTCACTTAAGG
 High quality sequence stop: 679.
 FEATURES
 source
 1..731
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEH009J22f"
 /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
 HVCNDA0009 (5 to 45 DAP)"
 /tissue_type="5-45 DAP spike"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 194 a 132 c 186 g 216 t 3 others
 ORIGIN
 Query Match 15.5%; Score 452.4; DB 137; Length 731;
 Best Local Similarity 77.2%; Pred. 1.2e-115;
 Matches 561; Conservative 0; Mismatches 164; Indels 2; Gaps 1;
 QY 1295 cttcaactgacacagggatcatgtgactcgtcttcaactatg 1354

Db 7 CTTTATGCGGCTCACGGGCACTGATGGGATTCCTGTTCACTACGCG 66
 QY 1355 gagctgggaagttcctaagttcttccttcctaataagcagagtggtgtagtacaa 1414
 Db 67 GAATGAAGAAAGTTAAAGGTTTACTTCCAAATGCCAGATGGGGCTTAGAATATA 126
 QY 1415 gtttagtggttcagatttgatggtggtgactcaatgatgacccatgatgtga 1474
 Db 127 GTTCCATGGGTTCCCATTCGACGGGCCCATCTCATATGATATACCCCATGATATCA 186
 QY 1475 gtagatttcaacgcaactcaatgaatacttgatgatatcaactatgtagtct 1534
 Db 187 AGTACCTT-ACAGAGACTACATGATATTTTGGCTTCCCGAGATGATGAGT 244
 QY 1535 ggttattatgctggttgaatgatalgatcatgctcctccagaggtgcacat 1594
 Db 245 TGTTCCTTGAATGCTGGTGAATGATCTAATTCACGCGCTTATCTGAACCGTTACTAT 304
 QY 1595 tggtagaagatgtagtgaatgcaacagcttgatccggtgtagaagtgtgtg 1654
 Db 305 TGTGTAAGATGTTAGTGAATGCTTACATTTGCCCTTCTGTTCAAGTGTGGGTTGG 364
 QY 1655 ctgtatattcgtctccacatgctgctgtgctgataaagtgtgtagatttcagaag 1714
 Db 365 TTTTGACTATGCTTACATGATGCGGCTTCCGATTAATGATTAATCTTCAAGAGAG 424
 QY 1715 agatgaagattggaataatggtgtgacattgtacatgctgacacagcgggtgtgga 1774
 Db 425 CGATCAAGGTTGGGAGATGGGTAAATTTGTCACACATAAATAATGAAGTGTGGA 484
 QY 1775 aaagtgtcttctatgctgaagatcagacagccctgtgtgtgacaaactatgc 1834
 Db 485 AAAGTGTCTTACTTATGCTGAAGCATGATCAAGCACTGTTGGAACAAGACTATTGC 544
 QY 1835 atttgcctgtagcaagaatgatgatgacttgcattgccttcacagacatctacc 1894
 Db 545 ATTGCGTGTATGAGCAAGATGATGATTTGATGCTGTGACGACCTTGACACC 604
 QY 1895 tctcatagatcgtgtagtagcatgacacaaatgatacaggttatccatgtagtag 1954
 Db 605 TAATATGATGTCGGAATATGACATCACTAAATGATTATGACATTCACATGCTTATG 664
 QY 1955 cgggaagatattgatttattgagaatgattgagaccccgagtgattgtt 2014
 Db 665 AGGAGAGGTTATCTTACTTATGGAATGAGTTCGGCATCTGATGATGACTN 724
 QY 2015 tccaaga 2021
 Db 725 TCCAAGA 731

RESULT 3
 BE195628 801 bp mRNA EST 02-MAR-2001
 LOCUS HVSMEH008P20f Hordeum vulgare 5-45 DAP spike EST library
 DEFINITION HVCNDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH008P20f,
 mRNA sequence.
 ACCESSION BE195628
 VERSION BE195628.2 GI:13188305
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 ; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 801)
 AUTHORS Wing,R., Close,T.J., Kleinof,A., Wise,R., Begum,D., Frisch,D., Yu
 ,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
 ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
 Wood,T.
 TITLE Development of a genetically and physically anchored EST resource
 for barley genomics

ORIGIN

Query Match 12.0%; Score 350; DB 167; Length 592;
 Best Local Similarity 74.5%; Pred. No. 6.2e-87;
 Matches 440; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

1847 ggacaagatattatgactcgtctcttgcaacacatctactccctcatagatcg 1906
 1 ggataagcattatgattatgctctgagatgacaccttcaactcctcgatgacg 60
 1907 tggagtagcattgacacaatgacagcttattacatgagatgagtcggaagata 1966
 61 tggcattacattatgataatgatacagcttgacacatgctggttagggcagctga 120
 1967 ttgcaatttatgggaatgaaatttgacaccccgagtgatgatttccaaagatga 2026
 121 tctttaaacttcaatggcaaatgagttgggacatcctgaatgagatgatttccaaagagctcc 180
 2027 tctacatctccagctgtaaatgttctctggaacaacattatgataaatgacg 2086
 181 gcaaaccttcttccacacggcgaatgctcccggaatgatacattatgataatgacg 240
 2087 ggcgtaggttgatcctgagcaatcaaacgacatcgtatgatacagatgaaagattga 2146
 241 ccgtagatttgaatcttgagatgacagatttcttgaatgacggtgagatgacagagcttga 300
 2147 tcaagcaattcagcacttggaagagcctatggttctgacatcttgagacacatacat 2206
 301 ccagcgaatgacgacatcttggaagaaatgagcttattgacatctgacacacagatgct 360
 2207 atcacggaagatgaaagagatcgatcgtctctggaagagaaacctgcttctgt 2266
 361 ttacaggaatgacgagaaatgagatgacatcttgcgaagagagatttggatttgg 420
 2267 atcaatttctgactgacagcactatggtgattacccgagttgctgtaagcagcg 2326
 421 ttttcaacttccactgagcgaatgagcttcttgaatgacggttggatgcttcaaacgcttg 480
 2327 aaagacagatgactgactgacatgacatcttctgttggaagcgttgagcgttag 2386
 481 gaagtcacaaagtgcttgaactccgacagatgacatcttntggatgacagcagcttga 540
 2387 tcatgtagcagagcactcagcttgaagagtgatgacataacgagcgtcg 2437
 541 tcatgtagtctactactcacaacgacacatccgacatgacatgacagcagc 591

RESULT 11
 BG551002 433 bp mRNA EST 09-APR-2001
 LOCUS sad31h09.y1 Gm-cl074 glycine max cDNA clone GENOME SYSTEMS CLONE
 DEFINITION ID: Gm-cl074-1914 5' similar to TR:09X1S5 09X1S5 BRANCHING ENZYME 1
 PRECURSOR: mRNA sequence.
 ACCESSION BG551002
 VERSION BG551002.1 GI:13562782
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
 1 (bases 1 to 433)
 Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna
 'A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
 'Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk
 'R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 'R., Waterston, R. and Wilson, R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project

FEATURES

source

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available through: Genome Systems, Inc. 4633 World
 Parkway Circle St. Louis, Missouri 63134 For further information
 call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
 427-3324 or contact: clones@genomesystems.com or
 info@genomesystems.com web site: www.genomesystems.com
 High quality sequence stop: 433.
 Location/Qualifiers
 1..433
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl074-1914"
 /clone_1db="Gm-cl074"
 /tissue_type="seedlings induced for HR (hypersensitive
 response)"
 /dev_stage="9-11 day old"
 /lab_host="DH10B"
 /note="Vector: Bluescript II SK(+). Site 1: EcoRI. Site 2:
 XhoI. The cDNA library was constructed from mRNA isolated
 from 9-11 day old seedlings by vacuum infiltration plant
 (hypersensitive response) by vacuum infiltration plant
 tissue with Pseudomonas syringae pv. glycinea carrying the
 avrB gene (Genetics 141:1597-1604). Plant tissue (expanded
 unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36,
 and 53 hrs after inoculation and their mRNA pooled equally
 for cDNA construction. The library was prepared using the
 Stratagene pBluescript II SK(+) library construction kit.
 Complementary DNA was synthesized from mRNA using a primer
 consisting of a poly(dT) sequence with an XhoI restriction
 site. EcoRI adaptors were ligated to the blunt-ended cDNA
 fragments followed by XhoI digestion. The cDNA insert is
 protected from XhoI digestion via methylation during first
 strand synthesis. The cDNA fragments were directionally
 cloned into the EcoRI-XhoI restriction site of the
 pBluescript vector. The ligated cDNA fragments were
 transformed into E. coli Electromax DH10B host cells. Plant
 care, inoculations, and library construction were
 performed by Steve Clough (Lila Vodkin lab, University of
 Illinois)."

BASE COUNT 121 a 71 c 115 g 126 t
 ORIGIN

Query Match 11.2%; Score 326; DB 155; Length 433;
 Best Local Similarity 84.9%; Pred. No. 3.1e-80;
 Matches 365; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

1609 gtggaatgccaacagcttgcattccggttggaagatggtggttggcttattatgc 1668
 3 gtggaatgccaacagcttgcattccggttggaagatggtggttggcttattatgc 62
 1669 tccacatgctgttctgctgataaatggttggaattatcagaagaagatgaattga 1728
 63 tgcacatggccattgacagacaaagctggtgacaaagcattgacaaagcattga 122
 1729 aaatgggtgacattgacacatgctgacacagagcggtggttggaaagtgcttct 1788
 123 aaatgggtgacattgacacatgctgacacagagcggtggttggaaagtgcttct 182
 1789 atgctgaagatcagacagagccttgttgggtgacaaactatgattgctgagtg 1848
 183 atgctgaagatcagacagagccttgttgggtgacaaactatgattgctgagtg 242
 1849 acaagatgattgattgattgattgattgattgattgattgattgattgattgattg 1908
 243 acaagatgattgattgattgattgattgattgattgattgattgattgattgattg 302
 1909 gattgattgattgattgattgattgattgattgattgattgattgattgattgattg 1968

Db 303 GTATAGCGTTGCACAAATGATTAGCTTATTACATGGCTCTTGCTGATGAAGGTATNT 362

QY 1969 tgaattcatggaagaatggaacacccagagtgatgattttccaagagtgatc 2028
 |||||

Db 363 TAATTTTATGGGATGATTTGGCCATCTGAGTGATGATTTCCAAAGGCGTGATC 422

QY 2029 taactcttc 2038
 |||||

Db 423 AACATCTTCC 432

RESULT 12

LOCUS BE517857 499 bp mRNA EST 08-AUG-2000

DEFINITION WHE0803_A06_B125 wheat vernalized crown cDNA library Triticum aestivum cDNA clone WHE0803_A06_B11, mRNA sequence.

ACCESSION BE517857

VERSION BE517857.1 GI:9741887

KEYWORDS EST

SOURCE bread wheat.

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticaceae; Triticum.

REFERENCE 1 (bases 1 to 499)
 Anderson O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsiao, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
 The structure and function of the expressed portion of the wheat genomes - Vernalized crown cDNA library
 Unpublished (2000)
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105959773
 Fax: 5105959818
 Email: oanderson@wpr.usda.gov
 Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
 Seq primer: Stratagene SK primer.

TITLE The structure and function of the expressed portion of the wheat genomes - Vernalized crown cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Olin Anderson

FEATURES

Source 1..499

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="WHE0803_A06_B11"

/clone_lib="Wheat vernalized crown cDNA library"

/tissue_type="Crown tissue of seedling"

/dev_stage="Five-week old seedling"

/lab_host="E. coli SOLR"

/note="Vector: lambda Uni-ZAP XR, excised phagemid; grown at 4 C for 5 weeks. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give Bluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 149 a 91 c 121 g 138 t

ORIGIN

Query Match 11.0%; Score 320.6; DB 136; Length 499;
 Best Local Similarity 78.6%; Pred. No. 1e-78;
 Matches 383; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1759 acagggcggtgtgtggaagaagtgttcttcatgctgaagcatgacagggcctgtgtg 1818
 |||||

Db 12 AAAAGAGGCTGCTGAGAGTGCCTACTTATGACGAAGAAGCATGATCAACACTAGTTG 71

QY 1819 gtgacaactatgcttgcgtgcatgagacaagatgatatgactcatgctctgt 1878

Db 72 GTACACAGACTATTTGCTATCTGTTGATGATAGATATGATGATTTTATGCTCTGG 131

QY 1879 acagaccactactcctctcatagatcgtgagtgatgcatcacaanaatgacagctta 1938
 |||||

Db 132 ATGACCTTCAACCTCTCGCATTTGATCGTGCAATGCAATTAATGATCAAGCCTTG 191

QY 1939 ttaccatggatlagcgagagaagatattgaattttaggaatgaatttgagacc 1998
 |||||

Db 192 TCACATGGGTTAGGTGGCGAAGCTTATCTTAATTATGGAATAGATTGGGATC 251

QY 1999 ccgagtgatgattttccaagagtgatcacaactcctccagtgtaatttgctctg 2058
 |||||

Db 252 CTGAATGATGATATTTTCCAAAGAGCTCCGCAACCTCTCCAAACCGCAAGTTCTCCCTG 311

QY 2059 ggaacaattacagttatataatgacgagtgagtgatttgatgaggaattcaagcatt 2118
 |||||

Db 312 GAATTAACAAATGATATATATAAATCCCGCTTAATTTGATGAGATCAAGATTTTC 371

QY 2119 tgaatatacaggaatgcaagagtttgatcaagaattcagcatctgaaagacattg 2178
 |||||

Db 372 TTAGATATCTGCTGATGCAAGAGTTCCAGCAGCAATGCAATCTTTGAGGAAAAATATG 431

QY 2179 gttcatgactctgagacacatcaatcaatcaggaagatgaaagagtcagatcattg 2238
 |||||

Db 432 GGTATATACATCTGACGACCATGATTTTCCGGAACATGAGGAATGAGTATGATCA 491

QY 2239 tcttcga 2245
 |||||

Db 492 TCTTCCA 498

RESULT 13

LOCUS A1795537 565 bp mRNA EST 02-FEB-2000

DEFINITION 605011A01.Y1 605 - Endosperm cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION A1795537

VERSION A1795537.1 GI:5343127

KEYWORDS EST

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 565)
 Walbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford University
 Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 605011 row: A column: 01.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

FEATURES

Source 1..565

/organism="Zea mays"

/cultivar="Ohio43"

/db_xref="taxon:4577"

/clone_lib="605 - Endosperm cDNA library from Schmidt lab"

/tissue_type="nucellar embryo, and endosperm"

/dev_stage="10-14 days post-pollination"

/lab_host="DH5(alpha)"

/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site: 1: Ecort; Site: 2: XhoI; Kernel endosperm cDNA library from Schmidt lab"

BASE COUNT 161 a 103 c 140 g 160 t 1 others

ORIGIN

Fri Aug 10 16:32:42 2001

us-09-297-703a-28.Aug9.rst

Page 14

ACCESSION	AI993785	sequence
VERSION	AI993785.1	
KEYWORDS	EST.	
SOURCE	thal. cress.	
ORGANISM	<i>Arabidopsis thaliana</i>	

ACCESSION CDNA clone 701514536, mRNA sequence.
VERSION AI993785
KEYWORDS AI993785.1 GI:5840690
SOURCE EST.
ORGANISM *thalassiosira weissflogii* (strain CC-114)
 thale cress
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 601)
REFERENCE Chen, J., Momiyama, M., Chan, E., Mooney, M., Carron, B., 2000. The
 cDNA sequence of the *Thalassiosira weissflogii* *CC-114* strain
 cDNA clone 701514536, mRNA sequence. *GenBank* accession
 number AI993785.1. <http://www.ncbi.nlm.nih.gov/Genbank/Genbank.html>

TITLE	Arabidopsis thaliana Gene Expression Microarray
JOURNAL	Unpublished (1999)
COMMENT	Contact: David Smoller, Ph.D.

Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com
www.genomesystems.com
Location/Qualifcare

BASE COUNT	174 a	146 c	145 g	136 t
ORIGIN	174 a	146 c	145 g	136 t

Search completed: August 10, 2001, 11:42:31
Job time: 6683 sec

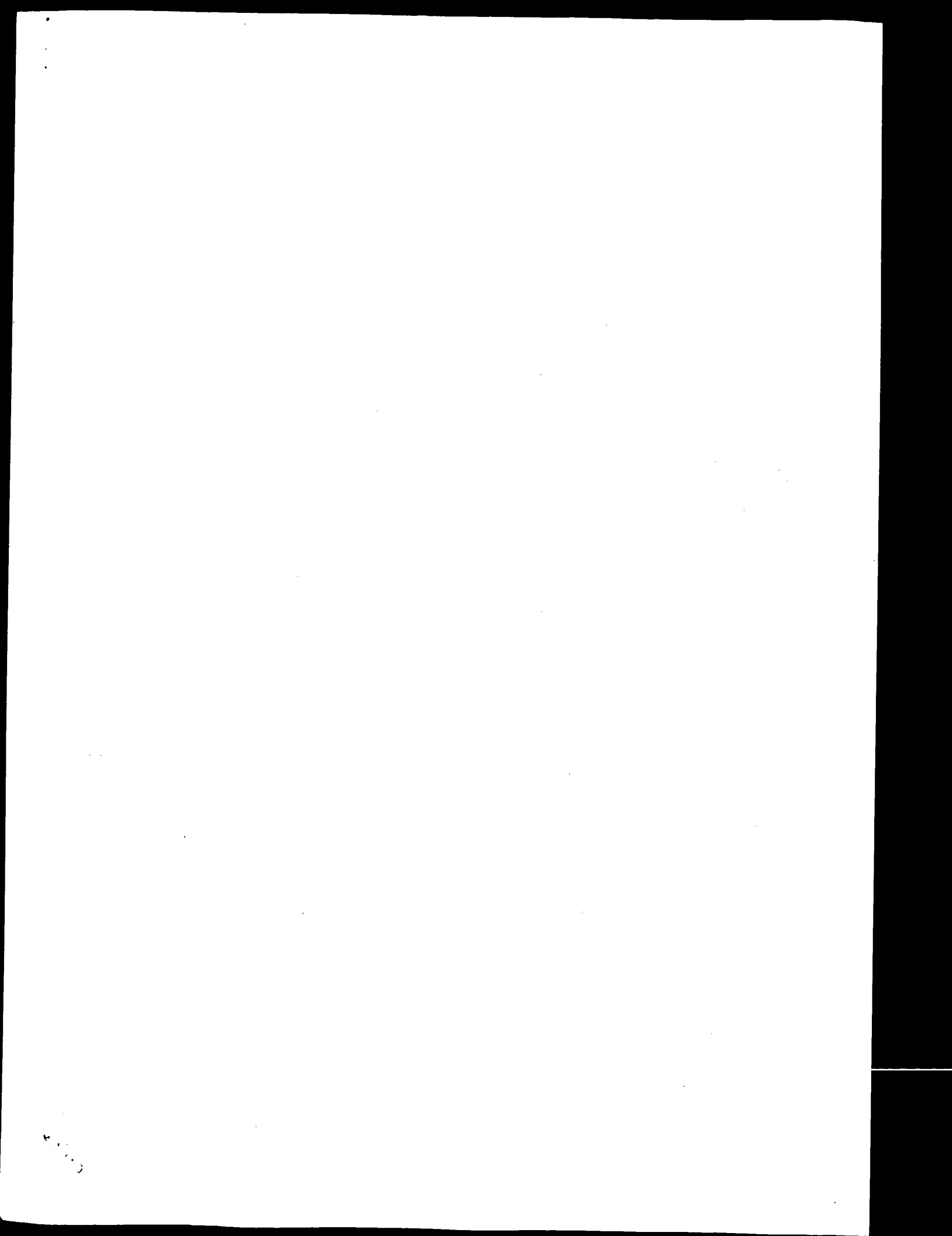
Query Match	10.6%;	Score 309.2;	DB 104;	Length 601;
Best Local Similarity	78.3%;	Pred. No. 1.8e-75;		
Matches 371;	Conservative	0;	Mismatches 103;	Indels 0

Dy 1575 ttccacagagcgtctcaccaattgltgaagaatglttagtgaagtgcacaagtttgacttcg 1634
| | | | |
Db 8 TACCCTGAAGCGAATTACCGTTGGTGAAGATGTTAGTGATGCCAACATTTCGTATCC 67
| | | | |
OY 1635 gttaagaatggtagtgtgtgtgcttgatacgtctccaatggtgtgtgtataatg 1694
| | | | |
Db 68 GTCCAAATAGTGGCGGTGGATTGCATACCGTTTACACTGGCCCATACCTATTAAGGG 127
| | | | |
OY 1695 gttgaagtatctaagaagaagatatgaatbtgaanaatggtgatcatgatcatagtgt 1754
| | | | |
Db 128 ATGAAATGCTCAAGAAGAGATGAAGACTGGCAATATGGCGCAGCATCATTTACACACT 187
| | | | |
OY 1755 accacaaggcggtgtgtgtgaagaagtgtgttcttatgtcgtgaafgcagaccagccct 1814
| | | | |
Db 188 ACCAAATAGAAGGGTGCACAGAGATGATACCTTATGCTGAAGTACAGATCAAGCTTT 247
| | | | |
OY 1815 gtctgtgacaaaacattgtcatttggctgtatgacaaagatalgtatgactcatgct 1874
| | | | |
Db 248 GTTGGTGAATAAACAATTGCCCTTCTGGTTAATGCAACAGATATGTTGATTTTCATGSCA 307
| | | | |
OY 1875 cttagacagacatactacctctcatagatcgtgaagtagatgtgacaaaatgatcagg 1934
| | | | |
Db 308 GTAGACAGACCATCAACTCCTCTTATGCATGAGAGATAGCTTTGCAAAAATGATTAAG 367
| | | | |
OY 1935 ctattacacatggaatggcgsgaagaagataattgaaatttlaabggnaatgaaatgtga 1994
| | | | |
Db 368 CTTATAACTATGGGATTAGCGGCGTGAAGGTACTTAATTTTGTGGAAACGAATTCGGG 427
| | | | |
OY 1995 caccccgagtgatgtattctccaagaagtgatcatcatcttcocagtgtaa 2048
| | | | |
Db 428 CATCCAGAAATGGCTTGATTTCCACGAGACCACGACAGCGCTCTCACGCCGACA 481

Fri Aug 10 16:32:42 2001

us-09-297-703a-28.Aug9.rst

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2001, 11:02:38 ; Search time 184.84 Seconds
(without alignments)
9895.463 Million cell updates/sec

Title: US-09-297-703a-28

Perfect score: 2913
Sequence: 1 cctctactcttcagcgaa.....aaaacaaaaaatccatg 2913

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SID8/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID8/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID8/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SID8/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SID8/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SID8/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /SID8/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SID8/gcgdata/geneseq/geneseq/NA1987.DAT.*
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11: /SID8/gcgdata/geneseq/geneseq/NA1990.DAT.*
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15: /SID8/gcgdata/geneseq/geneseq/NA1994.DAT.*
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21: /SID8/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SID8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2913	100.0	2913	19 AAV38719	Full length cassav
2	2028	69.6	3090	19 AAV38720	Full length cassav
3	1384	47.5	3074	18 AAT69587	Potato starch bran
4	1381.2	47.4	2578	17 AAT42631	Class A starch bra
5	1378.4	47.3	2531	17 AAT17267	Class A starch bra
6	1377.8	47.3	3231	17 AAT42632	Class A starch bra
7	1376.8	47.3	2529	17 AAT42637	Class A starch bra
8	1371.4	47.1	2715	21 AAT42639	Arabidopsis thalia
9	1367.2	46.9	2576	17 AAT42636	Class A starch bra
10	1364	46.8	3033	17 AAT42630	Class A starch bra
11	1357.8	46.6	3003	17 AAT42634	Class A starch bra

12	1341.2	46.0	2975	17 AAT42635	Class A starch bra
13	1298	44.6	2919	15 AAT073750	Rice starch branch
14	1292.6	44.4	3015	19 AAV05639	Rice type IV starch
15	1256.6	43.1	2640	19 AAV070961	DNA encoding maize
16	1251.8	43.0	2665	18 AAT69729	Plasmid pBE240 ins
17	1251.8	43.0	2725	19 AAV29757	Zea mays starch br
18	1194.8	41.0	2275	19 AAV38722	DNA encoding part
19	1098.4	37.7	2307	19 AAZ99938	Corn starch branch
20	1097	37.7	2087	18 AAT69737	Corn starch branch
21	1095.4	37.6	2165	18 AAT69736	Corn starch branch
22	1062.6	36.5	1069	19 AAV38721	Arabidopsis thalia
23	789.4	27.1	1452	21 AAC36957	Corn starch branch
24	633.4	21.7	2487	18 AAT69747	Corn starch branch
25	633.4	21.7	2565	18 AAT69752	Zea mays starch br
26	633.4	21.7	2763	19 AAT29758	Plasmid pBE5 ins
27	633.4	21.7	2771	13 AAT24257	Plasmid pBE5 ins
28	633.4	21.7	2772	18 AAT69740	Rice starch branch
29	627	21.5	2733	15 AAT69740	WSE I-D4 cDNA seq
30	625.2	21.5	2687	20 AAX34646	Potato starch bran
31	623.8	21.4	2733	15 AAT00774	DNA encoding maize
32	605.2	20.8	3128	19 AAT70962	Potato amylose-amy
33	592.4	20.3	2713	19 AAT70962	Corn starch branch
34	587.8	20.2	2909	13 AAT07778	Corn starch branch
35	546.8	18.8	1809	18 AAT69753	Maize starch branch
36	546.8	18.8	1865	18 AAT69748	Nucleotide sequenc
37	384.8	13.2	8119	21 AAZ35392	Rice starch branch
38	376.8	12.9	977	21 AAZ29947	Consensus sequence
39	376.8	12.9	12151	15 AAT062137	Nucleotide sequenc
40	376.2	12.9	1085	21 AAZ39962	Rice starch branch
41	373.6	12.8	979	21 AAZ39962	Rice starch branch
42	373.6	12.8	12151	15 AAT054676	Nucleotide sequenc
43	370.4	12.7	984	21 AAZ29946	Potato starch bran
44	369	12.7	11475	19 AAV54979	Full length potat
45	369	12.7	11478	18 AAT79784	

ALIGNMENTS

RESULT 1	
ID AAV38719 standard; cDNA; 2913 BP.	
AC AAV38719;	
XX	
DF 21-SEP-1998 (first entry)	
XX	
DE Full length cassava tuber cDNA in pSJ107.	
XX	
XX Starch branching enzyme; SBE; cassava: ss.	
KW	
XX	
OS Manihot esculenta.	
XX	
FH Key	Location/Qualifiers
FT CDS	21..2531
FT	/*tag= a
FT	/product= SBE II
XX	
PN WO9820145-A2.	
XX	
PD 14-MAY-1998.	
XX	
PF 04-NOV-1997; 97WO-GB03032.	
XX	
PR 05-NOV-1996; 96GB-0023095.	
XX	
PA (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.	
XX	
PI Jobling SA, Safford R.	
XX	
DR WPI: 1998-286958/25.	
XX	
P-PSDB; AAM62599.	
XX	

Class A starch bra
Rice starch branch
Rice type IV starch
DNA encoding maize
Plasmid pBE240 ins
Zea mays starch br
cDNA encoding part
DNA encoding part
Corn starch branch
Corn starch branch
Arabidopsis thalia
Corn starch branch
Zea mays starch br
Plasmid pBE5 ins
Plasmid pBE5 ins
Rice starch branch
WSE I-D4 cDNA seq
Potato starch bran
DNA encoding maize
Potato amylose-amy
Corn starch branch
Corn starch branch
Maize starch branch
Nucleotide sequenc
Rice starch branch
Consensus sequence
Nucleotide sequenc
Rice starch branch
Nucleotide sequenc
Potato starch bran
Full length potat

PF Starch branching gene from cassava - useful for producing altered
 PT plants giving modified starch
 XX
 XX Claim 2: Fig 4: 67bp; English.

CC The present sequence encodes starch branching enzyme (SBE) II. It
 CC was isolated from cassava tubers. The products can be used for
 CC producing plants having altered starch quantities and qualities.
 CC They can also be used for producing altered plants such as cassava,
 CC banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
 CC and rice plants.

XX Sequence 2913 BP: 818 A; 549 C; 680 G; 866 T; 0 other:

Query Match 100.0%; Score 2913; DB 19; Length 2913;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2913; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 ctctctaactctcagcgaatgaggaactacacatacagaatacgtttctctgtg 60
 QY 61 ctccactctgcaatctcaatctaccggtcttcacgtctacgagagaccctctgtgc 120
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 QY 121 ttctctcaactcagaagagcggtttctagagaggtctctctcggaaagcatctcatg 180
 Db 121 ttctctcaactcagaagagcggtttctagagaggtctctctcggaaagcatctcatg 180
 QY 181 aatctgacccccaatataatgagtcactgctctcaaaaaggtctctccggatgtctga 240
 Db 181 aatctgacccccaatataatgagtcactgctctcaaaaaggtctctccggatgtctga 240
 QY 241 ttgaatgcatctctctcacaacagatacgaatggaagccctggagacggtttcgaagaat 300
 Db 241 ttgaatgcatctctctcacaacagatacgaatggaagccctggagacggtttcgaagaat 300
 QY 301 cccaaggtctctactgagtttgaaggtctcattagatgagatgagatgttgaagaatgag 360
 Db 301 cccaaggtctctactgagtttgaaggtctcattagatgagatgagatgttgaagaatgag 360
 QY 361 taaataaagaatctgttccaaatgagcgaggaagcttaacacagaaaattggaactaaac 420
 Db 361 taaataaagaatctgttccaaatgagcgaggaagcttaacacagaaaattggaactaaac 420
 QY 421 caaggtcattctccaccacccggcagaggaaggaataatatacagatagatccaaagcttga 480
 Db 421 caaggtcattctccaccacccggcagaggaaggaataatatacagatagatccaaagcttga 480
 QY 481 caggtcttcgtcaaacactagattacgggtattcacaagtaacaagaagactccgagaagaa 540
 Db 481 caggtcttcgtcaaacactagattacgggtattcacaagtaacaagaagactccgagaagaa 540
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 Db 601 caagcagtgaaacaggaataactatagagagtgagcagcagagaggttaagtgtggtgat 660
 QY 661 tgaattggaattcacaactgaatcctaatgacagatgtcactgactcaagaatgagtg 720
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 QY 721 gtgtctggagagatcttctggcgaataatgagatggttcacacaaattcccaatggtt 780
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 Db 841 tcaagttcgaatcagaacacagagtgaaactcccaataatgacatacta:gatctc 900
 QY 901 ccgagagaggaagatgtgttcaaaaatccctcagcgaagagacaaatcctcttga 960
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 QY 1201 taggtctctctgttctcactgagatatgttcaatacagacatacgaacttaagcttgatg 1260
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 Db 1441 tgaattcaatgagttaacacacatgagatgagatgagatgagatgagatgagatgagatg 1500
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 Db 1501 aatacttggatgtgac 1560
 QY 1561 tgaattcagtgctctcctccacagagagctgtcaacacattggtgaagacgtttagtgaag 1620
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 QY 1621 cagtttgcattctccgtcttgaagatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1680
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 Db 1681 ttgcctgataaagt 1740
 QY 1741 ttgatacatgtgtgac 1800
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 QY 1801 atgacacagccctctgt 1860
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 QY 1861 atgacacttcatgt 1920
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Dp	1921	acaaaagacacagcgtattacacacagggatctggcgaggaagagatattgaatttag	1980
QY	1981	gaatgattctgacaccccgagctgagatcttccaaagagctgatactctcca	2040
Dp	1981	gaatgattctgacaccccgagctgagatcttccaaagagctgatactctcca	2040
QY	2041	gtcgtaaatgttctctgggaacaattaaagtatgataaattgcgcggtaggttgatc	2100
Dp	2041	gtcgtaaatgttctctgggaacaacaattaaagattagaataaagccggtaggttgatc	2100
QY	2101	taggaattcaaaagcattctgagatatactacagaaatgcaagagcttgatacgaattcagc	2160
Dp	2101	taggaattcaaaagcattctgagatatactacagaaatgcaagagcttgatacgaattcagc	2160
QY	2161	atctctgaagaagcctatgctgtttcatagctcttgagcacacaataacatcacagggaagt	2220
Dp	2161	atctctgaagaagcctatgctgtttcatagctcttgagcacacaataacacaggaagagt	2220
QY	2221	aaagagatcgatcatatgctcttcgagagagggaacctcgctttcttgatccaatttcatt	2280
Dp	2221	aaagagatcgatcatatgctcttcgagagagggaacctcgctttcttgatccaatttcatt	2280
QY	2281	ggactagcagcctattcggtattaccgggttgctgctgtcttaagccaggaagtacaagtag	2340
Dp	2281	ggactagcagcctattcggtattaccgggttgctgctgtcttaagccaggaagtacaagtag	2340
QY	2341	tcttgagttcaagatgaccccttgcttggagagccttgccagcagctctgatactgacagagc	2400
Dp	2341	tcttgagttcaagatgaccccttgcttggagagccttgccagcagctctgatactgacagagc	2400
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QY	2461	gtagaacacgacgtgactaagctctttagcttggaagatgaagctgagagatgaatttggaacctg	2520
Dp	2461	gtagaacacgacgtgactaagctctttagcttggaagatgaagctgagagatgaatttggaacctg	2520
QY	2521	tcgcgcggttaagagatatcttaacaacaggtcttcgaagaaggaatgccttaattgacct	2580
Dp	2521	tcgcgcggttaagagatatcttaacaacaggtcttcgaagaaggaatgccttaattgacct	2580
QY	2581	ccatgcttcacctcgtcttgagacgaatatattgagcctaataattgtagtgcacggtcctt	2640
Dp	2581	ccatgcttcacctcgtcttgagacgaatatattgagcctaataattgtagtgcacggtcctt	2640
QY	2641	gcagatttccatctcgtgttcttggtatttggttgataagataaacaataacaaagacaa	2700
Dp	2641	gcagatttccatctcgtgttcttggtatttggttgataagataaacaataacaaagacaa	2700
QY	2701	taggaagaacgacgggttcaatgctcagctccatcatatagggagacgaacctcttaaac	2760
Dp	2701	taggaagaacgacgggttcaatgctcagctccatcatatagggagacgaacctcttaaac	2760
QY	2761	cataaattccaagctcgcgtcgttggtgtagtattgtagttagttagttagttagttagttaa	2820
Dp	2761	cataaattccaagctcgcgtcgttggtgtagtattgtagttagttagttagttagttagttaa	2820
QY	2821	ttataatgacgcgtgtagatctgaacacatgacaatttgatataatgccaaggaagatt	2880
Dp	2821	ttataatgacgcgtgtagatctgaacacatgacaatttgatataatgccaaggaagatt	2880
QY	2881	taagtttaaaaaaaaaaaaaaaaaaaattcatg	2913
Dp	2881	taagtttttaaaaaaaaaaaaaaaaaaaattcatg	2913

RESULT	2
AAV38720	
ID	AAV38720 standard; DNA; 3090 BP

Accession	Gene Name	Location/Qualifiers
AAV38720;		
21-SEP-1998	(first entry)	
Full length cassava tuber cDNA in pS1146.		
Full length cassava tuber cDNA in pS1146.		
Starch branching enzyme; SBE; cassava; ss.		
Manihot esculenta.		
Key	Location/Qualifiers	
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CDS	131..2677	
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W09820145-A2.		
14-MAY-1998.		
04-NOV-1997;	97WO-GB03032.	
05-NOV-1996;	96GB-0023095.	
(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.		
Jobling SA, Safford R;		
WPI; 1998-286958/25.		
P-PSDB; AAW62600.		
Starch branching gene from cassava - useful for producing altered plants giving modified starch		
Claim 2; Fig 13; 67pp: English.		
The present sequence encodes starch branching enzyme (SBE) II. It was isolated from cassava tubers. The products can be used for producing plants having altered starch quantities and qualities. They can also be used for producing altered plants such as cassava, banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato and rice plants.		
Sequence 3090 BP; 877 A; 578 C; 721 G; 914 T; 0 other;		
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Best Local Similarity	88.3%; Pred. No. 0;	
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61 ----ctcacctctgcaatctcaatctcacgcgttcacatgctctcggaagactcttt 117		
171 cacttcaactctcaaatctcaatctcacgcgttcacatgctcggaagactctttcg 230		
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231 gcttctctctctctcgaagaagagcgctgttctctcgaagatcttgcggaagtc 290		
175 ctcattgaatctgactctcacaatgtaatgtaatgtaatgtaatgtaatgtaatg 231		
291 ctatgtaatctgactctcacaatgtaatgtaatgtaatgtaatgtaatgtaatg 350		
232 atgtgcatgtaatgtaatgtaatgtaatgtaatgtaatgtaatgtaatgtaatg 291		
351 atgatacatgtaatgtaatgtaatgtaatgtaatgtaatgtaatgtaatgtaatg 410		

Db	1637	accaggtatctctcccaatgcgagatgvgtggttgatgtgagttccaaatttgatgatt	1656
Oy	1427	cagatttgatgggttgagcttccaatgagtgaacccctcacttgatcgagtgatattac	1486
Db	1697	tagatttgatgggttgagctcactaatgatatgatactccacgagattatgcgtgagttcac	1726
Oy	1487	cgagcaatcaatgaataacttttgatagatagaatgataatgataatgctgtgattatgat	1546
Db	1757	tgaggaactacaggaataacttttgactgcgaactgtgagatgctgtgtgtatctgat	1816
Oy	1547	gctgttgatgatatgatttaattgctctctcccaagagctgtccaccttgatgaaagt	1606
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Db	1997	gagagttgggtgatatcttctcatcactgacgaataaataaagatgtgtcgaaagtgtgttc	2056
Oy	1787	ttatgctggaagatcatcacaagcgccctgtgtgtgtgacaaactatgtcatttgctcat	1846
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Db	2117	ggacaagaatgatgatgattttatgtgctctcggtgtagcctacatcatatataatagatcg	2176
Oy	1907	tgagatgagcttgacacaataatgatacggtctatccatcaggaatgaacggagaagata	1966
Db	2177	tgagatgagcttgacacaagaatgatacttgagctgtgtaactaaggatcaagagaggaagata	2236
Oy	1967	ttggaattttatgggaaatgaatttggacaaccccgagtgatatttttccaagaagtgtga	2026
Db	2237	ccataatctccatgggaaatgaatcttcggcaaccccgagtgatgttctcccaaggcgga	2296
Oy	2027	ttcatcatctcccaagtgtgtaaatgtgtctccctgggaacaattacagtatgataaattgcg	2086
Db	2297	acaacacctctcgtatgctgacgaataatctcccggaacccaattccatgtatgaataatgag	2356
Oy	2087	gcgttaggtttgatctagtgcaattccaagaactgagatactatgaaatgaagaagtgtga	2146
Db	2357	acggaagatcttgacctgggaaatgacaataatttaagaatacgttggtgtgcaagaatttga	2416
Oy	2147	tcaagcaattccagatctctgaaagaacgctatgtgttcaagactcttgagcaccacaataat	2206
Db	2417	ccggactatgcagatcatctctgaaagataaataatgatttcaagacttccagaacacagttcat	2476
Oy	2207	atcccggaagaagatgaagaagagatcgatgcatctgtcttcggaaggggaaacccgtgtttgt	2266
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Oy	2327	aaagtataaagatgcttgatgatactcaatgataactgtgtttggaagctttggcaagcttag	2386
Db	2597	aaataataaagttgaccttgactgaccagaatgataccacttttgggtgtccggagaattga	2656
Oy	2387	tcaatgacgcagagcacttcagctttgaagaagtgatgataacccgctcgatccctcat	2446
Db	2657	tcaataatggccgaataatcttccactcttgaaagaaatgataatgatacgtgtccctgtccaatat	2716
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Db 890 atattatgactcctccagagagagagatgctgctcagtcagacactccacatagatgac 949
QY 947 aaatcaactcgtgattatgagtcgacagtggtgagatgagtgagtcgagagcagatgaa 1006
Db 950 aaatcgtcgtgagatataatgataatcctcagatgagtgagtcgagagcagatgaa 1009
QY 1007 caactatgcacacttgaagaatgagtgctcctccagtcacaaagagtggtcacaatgac 1066
Db 1010 ctcatagtgagattttagagtgagtgagtgctcctccagtcacaaagagtggtcacaatgac 1069
QY 1067 tgttgaactgagtcacatcaagaagcattcatatagtgctggttgggtacagtcac 1126
Db 1070 ggtgcaaatgagtcacatcaagaagcattcatatagtgctggttgggtacagtcac 1129
QY 1127 aaacttgaatgagtcacatcaagaagcattcatatagtgctggttgggtacagtcac 1186
Db 1130 aaacttgaatgagtcacatcaagaagcattcatatagtgctggttgggtacagtcac 1189
QY 1187 taaagtcacagatgagtgcttctgttctcatagatattgttcatagacatgacatcaac 1246
Db 1190 taaagtcacagatgagtgcttctgttctcatagatattgttcatagacatgacatcaac 1249
QY 1247 taatagtcagtgagtcacatcaagaagcattcatatagtgctggttgggtacagtcac 1306
Db 1250 taatagtcagtgagtcacatcaagaagcattcatatagtgctggttgggtacagtcac 1309
QY 1307 accaagtgagtcacatcaagaagcattcatatagtgctggttgggtacagtcac 1366
Db 1310 accaagtgagtcacatcaagaagcattcatatagtgctggttgggtacagtcac 1369
QY 1367 tctaaagtgcttcttccaaatgcaagtggtggttgaagtcagtcacagtggttgggt 1426
Db 1370 tctaaagtgcttcttccaaatgcaagtggtggttgaagtcagtcacagtggttgggt 1429
QY 1427 cagattgagtgagtgagtcacatcaagaagcattcatatagtgctggttgggtac 1486
Db 1430 tagatttgagtgagtgagtcacatcaagaagcattcatatagtgctggttgggtac 1489
QY 1487 cggcaacaaatgagtcacatcaagaagcattcatatagtgctggttgggtac 1546
Db 1490 tgggaactacagagataacttgcagtcacatgagtggttgggtac 1549
QY 1547 gctgttgaatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1606
Db 1550 gctgttgaatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1609

QY 1607 tagtgagtgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1666
Db 1610 tagtgagtgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1669
QY 1667 tctcaacatgagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1726
Db 1670 gctgtcagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1729
QY 1727 gaaatgagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1786
Db 1730 gaaatgagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1789
QY 1787 ttagtgagtgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1846
Db 1790 ttagtgagtgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1849
QY 1847 ggaacagagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1906
Db 1850 ggaacagagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1909
QY 1907 tggagtagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1966
Db 1910 tggagtagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 1969
QY 1967 tttgagtagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2026
Db 1970 tttgagtagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2029
QY 2027 tctacatctccagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2086
Db 2030 tctacatctccagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2089
QY 2087 gctgagtagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2146
Db 2090 gctgagtagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2149
QY 2147 tcaagcaatcagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2206
Db 2150 tcaagcaatcagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2209
QY 2207 atcaggaagagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2266
Db 2210 atcaggaagagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2269
QY 2267 atcaggaagagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2326
Db 2270 atcaggaagagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2329
QY 2327 aaagtaacagatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2386
Db 2330 aaagtaacagatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2389
QY 2387 tcaatgagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2446
Db 2390 tcaatgagtcagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2449
QY 2447 ggtgtaacagatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2506
Db 2450 ggtgtaacagatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcacatgagtcac 2509
QY 2507 tgaatgag 2516
Db 2510 agaaagag 2519

RESULT 5
AAT17267
ID AAT17267 standard; DNA: 2531 BP.
XX
AC AAT17267;
XX
DF 03-MAR-1997 (first entry)

QY 947 aaatcattcgatattatgagtcgacgttggaatgagtagtagcagccgaatataa 1006
 Db 1256 aaatcgctgagatataatgattctatgagtagtagtagcagccgaatataa 1315
 QY 1007 cacaatgccaactttagatagatgagtcgcttcgcacatacaaaagcttgctacaatgc 1066
 Db 1316 ctatagctgagattttagagagtgagttcttcctcgacataaaaaacttggtagaactgc 1375
 QY 1067 tcttcagctgagtcgatttcaagagcattatattagcaggttttgagtagaactgc 1126
 Db 1376 gctgcaaatatgagctatctcaagccttcttataatgacagtttggtagaactgc 1435
 QY 1127 aaactttatgacatgacgagccgagcttggaactccgtagatataagctctaataga 1186
 Db 1436 aaatttttgacacacgagcgttcctggaacgcccgaacacctaagctcttgagtaga 1495
 QY 1187 taaagctcaagagtagagcttctgcttcgaatgagtagatgtagcagtagcagtaga 1246
 Db 1496 taaagctcaagagtagagcttctgcttcgaatgagtagatgtagcagtagcagtaga 1555
 QY 1247 taatacgttggatgagtcggaatattgtagatgtagcagtagcagtagcagtaga 1306
 Db 1556 taatacgttggatgagtcggaatattgtagatgtagcagtagcagtagcagtaga 1615
 QY 1307 acccagggggtatcatgagtagtgagacgtcgccttcgaactatgagagcctggagag 1366
 Db 1616 agctcggtgtagatcatgagtagtgagacgtcgccttcgaactatgagagcctggagag 1675
 QY 1367 tctaaagttcttccttcacaaatgagtagtgagtagtagtagtagtagtagtagtag 1426
 Db 1676 actaaagttcttccttcacaaatgagtagtgagtagtagtagtagtagtagtagtag 1735
 QY 1427 cagatttggagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1486
 Db 1736 tagatttggagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1795
 QY 1487 cggcaactacaagaatactttagatgtagtagtagtagtagtagtagtagtagtag 1546
 Db 1796 tgggaactacaagaatactttagatgtagtagtagtagtagtagtagtagtagtag 1855
 QY 1547 gctgttgaatgagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1606
 Db 1856 gctgttgaatgagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1915
 QY 1607 tagtggaaatgccaacagtttgcacgttcgagtagtagtagtagtagtagtagtagtag 1666
 Db 1916 tagtggaaatgccaacagtttgcacgttcgagtagtagtagtagtagtagtagtagtag 1975
 QY 1667 tctccacatgagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1726
 Db 1976 gctgcacatgagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2035
 QY 1727 gaaatgagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1786
 Db 2036 gaaatgagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2095
 QY 1787 ttatgtagaaatgtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1846
 Db 2096 ttatgtagaaatgtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2155
 QY 1847 gggcaagagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1906
 Db 2156 gggcaagagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2215
 QY 1907 tggagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1966
 Db 2216 tggagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2275
 QY 1967 ttggaattttagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2026
 Db 2276 cctaaattttagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2335
 QY 2027 tctacattctccagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2086

Db 2336 acaacacccctctgtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2395
 QY 2087 ggttag 2146
 Db 2396 agggagtag 2455
 QY 2147 tcaagtag 2206
 Db 2456 cgggtag 2515
 QY 2207 atccggaagtag 2266
 Db 2516 atccggaagtag 2575
 QY 2267 attcaatttctgtag 2326
 Db 2576 attcaatttctgtag 2635
 QY 2327 aaagtag 2386
 Db 2636 aaagtag 2695
 QY 2387 tcatgtag 2446
 Db 2696 tcatgtag 2755
 QY 2447 ggttag 2506
 Db 2756 ggttag 2815
 QY 2507 tgaattgtag 2566
 Db 2816 tgaattgtag 2875
 QY 2567 ccaat 2571
 Db 2876 gctgt 2880

RESULT 7
 AAT42637
 ID AAT42637 standard; DNA: 2529 BP.
 AC AAT42637;
 DE 03-MAR-1997 (first entry)
 XX
 XX Class A starch branching enzyme (pcrsb2con.seq) cloned in Q832.
 XX Starch branching enzyme: SBE; class A; class B; Solanum tuberosum;
 KW amylose; viscosity; potato; ss.
 XX Solanum tuberosum.
 OS
 PN W09634968-A2.
 PD 07-NOV-1996.
 XX
 XX 03-MAY-1996; 96WO-GB01075.
 XX 10-APR-1996; 96GB-0007409.
 PR 05-MAY-1995; 95GB-0009229.
 XX
 XX (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX Cooke D., Debet M., Gidley M., Jobling SA., Safford R;
 PI Sidedotom CM, Westcott RJ;
 DR WPI: 1996-506170/50.
 XX
 PT New potato plant starch having high amylose content - also class A
 starch branching enzyme and corresp. DNA to alter the viscosity of

QY 2327 aaagatacaagatgcttgatcagatgacatccttctgttgagagcttggcagcttag 2386
 Db 2323 aaatacaaggttgcttgactgactgactcacttctgttgagagcttggcagcttag 2382
 QY 2387 tcatgatcagagcagcacttgcagcttgaaggttgctgacgaacgcctcagatccat 2446
 Db 2383 tcaatacgcgaatttccactctcgaagatcgtatgatacgtccctcgttcaat 2442
 QY 2447 ggtgtacacccatgtgagacacatgctgtctgtttagtgaggagatgaagtgaaga 2506
 Db 2443 ggtgtacacccatgtgagacacatgctgtctgtttagtgaggagatgaagtgaaga 2502
 QY 2507 tgatttgagaccctgctgcggttaa 2531
 Db 2503 agaaagaagaagaacccgmgagaaga 2527

 RESULT 8
 AAC45939 standard; DNA; 2715 BP.
 ID AAC45939.
 AC AAC45939.
 AT 18-OCT-2000 (first entry)
 DT
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48320.
 XX
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 PD 06-SEP-2000.
 XX
 XX 25-FEB-2000; 2000EP-0301439.
 PF
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
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 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
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 PR 06-MAY-1999; 99US-0132485.
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 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134256.
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 PR 28-JUN-1999; 99US-0140695.
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 PR 30-JUN-1999; 99US-0140991.
 PR 01-JUL-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
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PR	31-AUG-1999;	99US-0151348;
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PR	28-OCT-1999;	99US-0161992;
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[illegible]

Oy	2211	cgaaagatgaaagggatctcgatcatgtctcttcgaagaggaacotcgtttgtatc	2270
Db	2233	cgcagaagtgaagagcagcagatcatgtatcttcgaagaggttaactgtctcttc	2292
Oy	2271	aatttcattggtactgacgactatctcgattaccgaagttgcgtcttaagccctgaaag	2330
Db	2293	aacttccctcgtgaccacaacatctcctcgataccgatalctcgtctgtccctcgtgaaag	2352
Oy	2331	tacaagaatgacttggtattcaagaatgactcctctgttttggagcctttggcaagcttaagtc	2390
Db	2353	tacaaaatcgttttggactctgtataactctctttatttggagccttacaacggtctaatgatac	2412
Oy	2391	gatcacagacactcagcttttgaaggtctgtaacataaacggccctgcattcttaatgtg	2450
Db	2413	tcgcggaagtttccactctctgtatgtaaggaagacagataagcctctgcctcttaatgtg	2472
Oy	2451	tacaacacatgttgaagaagatggtcctatgctttcttgatgaagatgaagtgtgaatgaa	2510
Db	2473	tatgcacacgtgacaacacgctctgaattcttaacgtcgcagatagaagaagaatgataa	2532
Oy	2511	ttgaaacctgtgcgcggtttaaatatatactttaacaacagttcttgaacgaagaaatgtccat	2570
Db	2533	cgtctctctctgtcccacaagaagccgttaaccgaaagatgtttaaagacaagaacagctg	2592
Oy	2571	tattgatcttcctatgttcatctgcgtttgaagaaatatatgagccataatitgagt	2630
Db	2593	tcgaagttaactactgttaagctctcttctgttaactacaanaattactcgttgatattcttc	2652
Oy	2631	caaggtccttgacagattc	2669
Db	2653	tccttgaatttcgcttgc	2671

RESULT 9

ID AAT42636 standard; DNA; 2576 BP

AC AA142636;

DT 03-MAR-1997 (first entry)

DE Class A starch branching enzyme (86con.seq) cloned in QE32.

KW Starch branching enzyme; SBE; class A; class B, *Solanum tuberosum*,
 KW amylose; viscosity; potato; ss.

OS Solanum tuberosum.

PN W09634968-A2

PD 07-NOV-1996.

PF 03-MAY-1996; 96WO-GB01075.

PR 10-APR-1996; 96GB-0007409.

[illegible][illegible]

PI Sidebottom CM, Westcott RJ;
COOK D, Debel M, Staley MO,
Sidebottom CM, Westcott RJ;

DR WPI; 1996-506170/50.

AA	YY	Pt	New potato plant stage
1	1	1	1
2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
8	8	8	8
9	9	9	9
10	10	10	10
11	11	11	11
12	12	12	12
13	13	13	13
14	14	14	14
15	15	15	15
16	16	16	16
17	17	17	17
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19	19	19	19
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21	21	21	21
22	22	22	22
23	23	23	23
24	24	24	24
25	25	25	25
26	26	26	26
27	27	27	27
28	28	28	28
29	29	29	29
30	30	30	30
31	31	31	31
32	32	32	32
33	33	33	33
34	34	34	34
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37	37	37	37
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47	47	47	47
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49	49	49	49
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88	88	88	88
89	89	89	89
90	90	90	90
91	91	91	91
92	92	92	92
93	93	93	93
94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

PT starch branching enzyme

XX Example 1: Page 49-51: 142pp: English
PS

Class A starch branching enzyme (SBE) has been obtained from

CC potatoes. In class A SBE mols., a flexible N-terminal domain, CC is found which is not found in class B mols.

Db	2308	tcaataagccgaatattcaacettitgaagatgtagttagtgcgtcccgltcaatat	2447
Qy	2447	gggttaccacacagatgtagaacacagatgctctctctgcttaagtggagagatgaagtcgagaa	2506
Db	2448	gggtctatgcacactctgtcagacaacagatgctctctgcttaagtgaagaaagaa	2507
Qy	2507	tgaattcgaa	2516
Db	2508	agaagaagaa	2517

```

RESULT 10
AAT42630
ID AAT42630 standard; DNA; 3033 BP

```

DT 25-FEB-1997 (first entry)
 XX Class A starch branching enzyme (19con.seq).
 DE Starch branching enzyme; SBE; Class A; Solanum tuberosum
 XX anylose; viscosity; potato; ss.
 KW Solanum tuberosum.
 SS Solanum tuberosum.

	Key	Location/Qualifiers
FH	CDS	145..2793
FT		/*tag= a
FT	sig_peptide	145..288
FT		/*tag= b
FT	mat_peptide	289..2790
FT		/*tag= c
XX		
PN	W09634968-A2.	

XX 03-MAY-1996; 96WO-GB01075.
XX 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
XX (NATLT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R
PI Sleebottom CM, Westcott RJ;
XX
XX WPI; 1996-506170/50.
DR P-PSDB; AAM06399.

PT New potato plant starch having high amylose content - also class of
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
PS Claim 28-30; Page 42-46; 142pp: English.

CC Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain
CC is found, which is not found in class B mols.

XX Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;

Query Match	46.8%	Score 1364	DB 17	Length 3033
Best Local Similarity	75.9%	Pred. NO. 0		
Matches 1685; Conservative	0	Mismatches 535	Indels 0	Gaps 0

[illegible]

Db	633	tgatagatcagagagagagggcaccctccacccctgagcttggccagaaagatttaagaaat	692
Qy	467	agatccaaagcttgacagagcttctgtccaacacctagatattacggttatccaaagtaaaaag	526
Db	693	aaacccctcttgaaaacattctgcacaacaccttgatataaggtattccaaagtaaaaagaa	752
Qy	527	actccgagaagaatttgacaagatagaaggtatgtctgagbcaatttctctggtcgtataga	586
Db	753	actgagggagagcaattgacaagatagaaggttgggttttgaaagccctttctcgtgtattaga	812
Qy	587	aaagtttggttcttcacgcacgaatgaaaacagaaataaactatagaagagtgggcacacagagc	646
Db	813	aaaaatgggttcttcactcgttagtgcataacaggtatcacactaccgtaggtgggcctccgtgtgc	872
Qy	647	tacgtagggtctcatlgtatctgagatttccaataactggaactggaacccaaatgacagatgcatagac	706
Db	873	ccagatcagctgcctccatcttgagattccaacaattgggaacgaatgctgaaacatagac	932
Qy	707	tcaagaatgaagtggtgtgtctctgagagatccttttgcgcgaataaagcagatggttcacaccc	766
Db	933	tcgagatgaatttggctgtcgtggagatatttctgcacaataaagtgtgagtgtctctcgtgc	992
Qy	767	aattcccaatggtctctcgagaagaagatagcagatgagatctcatctctgcgaacaagaagatctc	826
Db	993	aattcctcatggtctccagagtgaaagatagtgatggacactccatcagcgtgttaagattc	1052
Qy	827	tattccgtcttgagatcgaagttccagttccagttccaagaacagaggtgaactccctcaataatggat	886
Db	1053	catctcgtcttgagatccaactacactctttaacgctctctgtgaatattccatatataggat	1112
Qy	887	atacctatgactctccgcagagagaggaagtatgtgttccaataaactccacgcacaaagagcc	946
Db	1113	acatatatgactccaccgcagagagagaggtatctactccaaacccacgcgcacaaagaac	1172
Qy	947	aaaatcactctcgatttatagaatctgcgcagcttggaaatgagtatgaogagagcagtaattaa	1006
Db	1173	aaagtcgcgtcgaaataatagtaaaatcccatatttgaaagagtagtcggagaccataaattaa	1232
Qy	1007	cacatagccaactttagagatagatgtgtctctccctcgatccaataaagcttggcttcaatgac	1066
Db	1233	ctcaatcgtgaattcttgagatgtagagttctctctccgataaaaagcttgggttcaaatgac	1292
Qy	1067	tgttcagctctatggtctatccaagaagcatataatttgcctaggttttgggtatccmctgtaac	1136
Db	1293	gctgcaaaattatggtctatccaagaagcatcttatttaacgtatgttgggtatccmctgtaac	1352
Qy	1127	aaactttatgacgtatgacgcagccgacttttgaaactctgtatgttaaaagtcctcctaataga	1166
Db	1353	aaatttttttcacacaagacgcgcttcttggaaacgcgcagacacttaagctcttcttgatga	1432
Qy	1187	taaaactcaacagatgaagctctctctgtgttcacagatatgttcatatagacatgaatccaac	1246
Db	1413	taaaagctcatagcttagaattgtgtcttcacatgagcatgtgttccaacagatgaatccaa	1472
Qy	1247	taataagcttgaatgggtctgataatgttttagatgtgaacgtgttcaactacttccactctg	1306
Db	1473	taaatcctttagatgtagtgaacatggttttagcctgcacgcgtagtgttacttctctctcgtg	1532
Qy	1307	acacgcgggtcatcatatgagatgttggagacctctgccttccaactatggaaagcttggaggt	1366
Db	1533	agctcgtgtgtatcatatgagatgttgggtatccgcctctttaaactatgaaacttggagaggt	1592
Qy	1367	ctctaagttcttcttccaatcaatcaaggttggtgtgtgtatgagttacaaagtttgatgggt	1426
Db	1593	actttaggaactctctcccaaatgcgaaatgaggttggtgtgtgtgtcccaaatcttgatggagct	1652
Qy	1427	cagatttgaatgggtgactctcaatgatgtaacccaatcaatgagatgcaggtatgaatttaac	1486
Db	1653	tagatttgaatgggtgactcaatgatgtaattatattcaacccagatcatcoggtgtgtatccac	1712
Qy	1487	cggagacacacaatgaacttcttgatatacnaatgtgataatgtgtgtgtgtttttttat	1546

Db 1713 tgggaactacaggaatacttggactcgcgaactgagtgtgtgtatctgat 1772
 QY 1547 gctgtgaatagatatgatacttgccttcccgaggctgtcccatgttgaaatgtc 1606
 Db 1773 gctgtgaacagcatcttacttgccttcccgaggctgtcccatgttgaaatgtc 1832
 QY 1607 tagtgaatgcgaacagtttgcattcgcgttgaagatgtgtgtgtgtgtgtgtgtc 1666
 Db 1833 tagcgaatgcgcgaacatttgcattcgcgttgaagatgtgtgtgtgtgtgtgtc 1832
 QY 1667 tctccacatggctgtc 1726
 Db 1893 gctgtgaatgcgaacatttgcattcgcgttgaagatgtgtgtgtgtgtgtgtgtc 1952
 QY 1727 gaaatgtgtgaatgtc 1786
 Db 1953 gaaatgtgtgaatgtc 2012
 QY 1787 ttaagctgaagatgcgaacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 1846
 Db 2013 atagctgaagatgcgaacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 2072
 QY 1847 ggaacagatagatgtc 1906
 Db 2073 ggaacagatagatgtc 2132
 QY 1907 tggatgaatgcgaacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 1966
 Db 2133 tggatgaatgcgaacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 2192
 QY 1967 ttggaatgtgaatgtc 2026
 Db 2193 tgaatgtgtgaatgtc 2252
 QY 2027 tctacatctccagtggtc 2086
 Db 2253 acaacatctctgtc 2312
 QY 2087 gctgtc 2146
 Db 2313 acggaatgtc 2372
 QY 2147 tcaagcaatctgaacatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 2206
 Db 2373 ccggcctatgcgaatctgtc 2432
 QY 2207 atcaggaagatgtc 2286
 Db 2433 atcaggaagatgtc 2492
 QY 2267 atcaatttcaatgtc 2326
 Db 2493 cttaatttcaatgtc 2552
 QY 2327 aaagcaagatgtc 2386
 Db 2553 aaagcaagatgtc 2612
 QY 2387 tcaatgaatgcgaacatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 2446
 Db 2613 tcaatgaatgcgaacatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 2672
 QY 2447 ggtgtgaacacatgtc 2506
 Db 2673 ggtgtgaacacatgtc 2732
 QY 2507 tgaatgtgaacatgtc 2566
 Db 2733 tgaatgtgaacatgtc 2792

RESULT 11
 AAT42634

ID AAT42634 standard; DNA; 3003 BP.
 XX
 AC AAT42634:
 XX
 DT 03-MAR-1997 (first entry)
 XX
 DE Class A starch branching enzyme (10con.seq).
 XX
 KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
 KM amylose; viscosity; potato; ss.
 XX
 OS Solanum tuberosum.
 XX
 PN MO9634968-AZ.
 PD 07-NOV-1996.
 XX
 PF 03-MAY-1996; 96MO-GB01075.
 XX
 PR 10-APR-1996; 96GB-0007409.
 PR 05-MAY-1995; 95GB-0009229.
 PA (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX
 PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
 PI Sidebottom CM, Westcott RJ;
 DR WPI; 1996-506170/50.
 XX
 PT New potato plant starch having high amylose content - also class A
 PT starch branching enzyme and corresp. DNA to alter the viscosity of
 PT starch; for use in food, biodegradable products, adhesives, etc.
 XX
 PS Example 1; Page 38-39; 142pp; English.
 XX
 CC Class A starch branching enzyme (SBE) has been obtained from
 CC potatoes. In class A SBE mols., a flexible N-terminal domain,
 CC is found, which is not found in class B mols.
 XX
 SQ Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;
 Query Match 46.6%; Score 1357.8; DB 17; Length 3003;
 Best Local Similarity 76.3%; Pred. No. 0;
 Matches 1682; Conservative 0; Mismatches 522; Indels 1; Gaps 1;
 QY 347 tgttgaagatgaatgaatgaatgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 406
 Db 571 tgttgaagatgaatgaatgaatgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 630
 QY 407 aatgtc 466
 Db 631 tgaatgaatgaatgaatgaatgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 690
 QY 467 agatcgaatgtc 526
 Db 691 agatcgaatgtc 750
 QY 527 actcgaagaatgtc 586
 Db 751 actcgaagaatgtc 810
 QY 587 aagttgtc 646
 Db 811 aagttgtc 870
 QY 647 taatgtc 706
 Db 871 taatgtc 930
 QY 707 tcaatgaatgtc 766
 Db 931 tcaatgaatgtc 990

XX 04-APR-1997; 97US-0042939.
PR
XX (EXSE-) EXSEED GENETICS LLC.
PA
XX Guan H, Keeling PJ;
XX MPI; 1998-568285/48.
DR P-PSDB; AAW70895.
XX
PT Producing non-glycogen-like polysaccharides in bacteria, fungi or
PT plants - transformed with genes for enzymes involved in starch or
PT glycogen synthesis allows fermentative production of starches with
PT engineered properties
XX
PS Disclosure; Fig 53; 150pp; English.
XX
XX The specification describes a method for the production of
CC non-glycogen-like polysaccharides in a host. The method comprises
CC transforming a host, suitable for fermentation, with genes encoding
CC starch- or glycogen-synthesis enzymes, and fermenting the transformants.
CC The specification also describes hosts transformed with a gene active
CC in glycogen synthesis and at least one non-starch branching gene.
CC involved in production of amylopectin or amylose in its original host.
CC The method is used to produce plant-like starches by fermentation and
CC new starches in plants. These starches are useful for all food and
CC non-food applications of starch. The present sequence is used in
CC the course of the invention.
XX
SQ Sequence 2640 BP; 715 A; 510 C; 686 G; 729 T; 0 other;

Query Match 43.1%; Score 1256.6; DB 19; Length 2640;
Best Local Similarity 75.6%; Pred. No. 0;
Matches 1559; Conservative 0; Mismatches 504; Indels 0; Gaps 0;

QY 430 ttctccaccgagcaggaagaaatataatagacatgacgaagcttgacagcttc 489
DB 340 tccccaccacgaagcagtaacaaatattccagattgaccccatggttgcaaggtata 399
QY 490 gtcaaacactagttccggtatccagtaacaaagactccgagagaatagacaagt 549
DB 400 agtacacacttgatcgtgtaacagcctctatagaagaatccgttcagacattgatac 459
QY 550 atgaagtagtctgtagtatttccgtgctatgaagaagcttggttcacagctg 609
DB 460 atgaagtagtctgtagtatttccgtgctatgaagaagcttggttcacagctg 519
QY 610 aacacgaataactatagaagtgaggacgaagctacgttggtcattgattgag 669
DB 520 cggaaaggtatcacatatacgatagtgctcctggagcatttctcgagattggtggtg 579
QY 670 attcaataactggaatcctaatgacagatgacatgacatgaatgagtggtgctggg 729
DB 580 actcaacaactggtgacatgaatgacagatgacatgacatgaatgagtggtgctggg 639
QY 730 agatcttttgcgaataatgacagatggttccacacaaatctcccaatggttcgaatga 789
DB 640 aaatttctgcgaataatgacagatggttccacacaaatctcccaatggttcgaatga 699
QY 790 agatacgcattgatactcattctgcaacaaagattcttccgtcgttgatcaatgctc 849
DB 700 aggtgagaatgatactcattctgcaacaaagattcttccgtcgttgatcaatgctc 759
QY 850 cagttcaacacagcagtgtagctccatataatgcatataactatgactccctccgagag 909
DB 760 cagttcagagcagcagtgtagctccatataatgcatataactatgactccctccgagag 819
QY 910 aagaatgattgttcaaaaatctcagccaaagacaaacaaatcactcgtgatttgagt 969
DB 820 taagaatgattgttcaaaaatctcagccaaagacaaacaaatcactcgtgatttgagt 879
QY 970 cgcagcttggaatgattgtagcagagccagtaataacacatatacgcaactttagagatg 1029

DB 880 cacatgtcggaatgtagcccggaacgaagaataacacatatactttagagatg 939
QY 1030 atgtgttctctgcatacaaaagcttgctacatgctgttcaagctcgtgcttaacag 1089
DB 940 aagttctcccaagaataaaaaaacttgtagatgacagcgttgcaaatatggaatccag 999
QY 1090 agacttcaataatgtagtatttggttgcacgttcacaaactttatgacagtagcagcc 1149
DB 1000 agcactcaatattatgaaactttgtagacacatgtaacttaatttttttgcgaagtagc 1059
QY 1150 gatttggaaactctatgattttaaagttctatagataagatcagacagtttagcttc 1209
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QY 1210 ttgttctcagatattgttcaatacagtcacaaactacatgcttgatgagcgtgaata 1269
DB 1120 tagctctcagatattgttcaatacagtcacaaactacatgcttgatgagcgtgaata 1179
QY 1270 ttgttgaatgtagcagatgtagtactcattcactctgacacaggggttcattgattgt 1329
DB 1180 gtttgaatgtagcagatgtagtactcattcactctgacacaggggttcattgattgt 1239
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QY 1390 caaagtgtgtgttgtagtagtaacagtttgatggttcaattgattgaggttgactcaa 1449
DB 1300 ctagaatgtgtgttgtagtagtaacagtttgatggttcaattgattgaggttgactcaa 1359
QY 1450 tgaatgaacacatattgattgtagcaggttagattttaccggaactacaatgaatactgt 1509
DB 1360 tgaatgaacacatattgattgtagcaggttagattttaccggaactacaatgaatactgt 1419
QY 1510 gatacgaactgtagtagatgctgtgtgttattgattgctgttgaatgattgattgt 1569
DB 1420 gcttgcacacagatgtagtagatgctgtgtgttattgattgctgttgaatgattgattgt 1479
QY 1570 gtcttcccaagagcgttccacattggttgaagatgtagtgaatgccaacagtttgca 1629
DB 1480 gacttatacctgagcgttgaacattggttgaagatgtagtgaatgccaacagtttgca 1539
QY 1630 ttccggtgaagatgtagtgtgtgtgttattgattgctgttccacatggtgttgcata 1689
DB 1540 ttccggtgaagatgtagtgtgtgtgttattgattgctgttccacatggtgttgcata 1599
QY 1690 aatggttgaatatttcaagaagagatgtagaatttgaaatggtgacattgacata 1749
DB 1600 aatggttgaatatttcaagaagagatgtagaatttgaaatggtgacattgacata 1659
QY 1750 tgcgtaccaaagcagcgtgtgttggaagagtgcttcttattgctgaagatgacagag 1809
DB 1660 cactgcaaaaatagagagtggttgaagagtgcttcttattgctgaagatgacagag 1719
QY 1810 cccctgtgtgtagcaaaaactatgatttgcgtgtagtgaagagatgattatgacttca 1869
DB 1720 cattagctggagcaagaactatgctgtgttgtagtgaagagatgattatgacttca 1779
QY 1870 ttgctttagacagacatctactcctcactagatcgttgtagtgaagatgacacaaatga 1929
DB 1780 ttgctttagacagacatctactcctcactagatcgttgtagtgaagatgacacaaatga 1839
QY 1930 tcaagcttattacatgtagttagcggagagagatatttgaattttagtgaagatgag 1989
DB 1840 ttagattatlaacaatggtttaggagagaggtctacttcttaatttcatggaatgag 1899
QY 1990 ttggaaccccgagtgtagtatttccaaagagtgtagtcaactcttccagtgagtaat 2049
DB 1900 ttggaaccccgagtgtagtatttccaaagagtgtagtcaactcttccagtgagtaat 1959
QY 2050 ttggtcctgggaacaattacagttatagataatgacggcgttaggtttagacttaggaat 2109

Fri Aug 10 16:32:39 2001

us-09-297-703a-28.Aug9.rng

Page 24

Db 1960 ttatccagggaataacaacaggtatgacaaatgtcgtcgaaagatttgacctggtgagt 2019
QY 2110 caaagcatctgagatatactggaatgcagaagatttgatcagaagcaattcagcatcttgag 2169
Db 2020 cagactatcttagtalcattgtaacagagatttgatcagaagcaatgcacatcttgagc 2079
QY 2170 aagcctatggttctgactcttgagcaaccaatatacatcacggaaggatgaaaggatc 2229
Db 2080 aaaaatataatcattgacatctgacccagatataattcccggaacacatgaggagata 2139
QY 2230 ggaatcatgctctcgagaagggaacccgtcttctgatatccaatttcattgactaga 2289
Db 2140 aggtgattgtgtcgaaaaggagatttgtaattgtgttcaacttccactgcacacaaca 2199
QY 2290 gctatcgattaccgagttgctgcttaagccaggaagacagataagtaagtccttgat 2349
Db 2200 gctatttgactacccgtaattgtgtcgaaagccctgggtgtatagtggtccttgact 2259
QY 2350 cagatgatccttgttttgagagccttgagagcttagtcatgatgacagacattcaagt 2409
Db 2260 ccgacgctgactatttgggtgatttagcagagatcatcagcagccgacattccacg 2319
QY 2410 ttgaaggtggtacgtaacccgacctcgatccttcattatggtgafacacacatgtagaag 2469
Db 2320 ccgactgttcgcatgataataaggccatatattctcgtttatacaccagaagacaacat 2379
QY 2470 cagtgtctatgctttagtgag 2492
Db 2380 gtgcgtctatgtccagtcgag 2402

Search completed: August 10, 2001, 12:53:48
Job time: 6670 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2001, 11:01:18 ; Search time 86.98 Seconds
(without alignments)
6340.116 Million cell updates/sec

Title: US-09-297-703a-28

Perfect score: 2913
Sequence: 1 cctctaacttcagcgaa.....aaaacacacacacacatcatg 2913

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1382.4	47.5	3074	US-09-087-277-1	Sequence 1, Appl1
2	1251.8	43.0	2725	US-08-941-445A-14	Sequence 14, Appl1
3	947.4	32.5	1393	US-09-087-277-3	Sequence 3, Appl1
4	633.4	21.7	2763	US-08-941-445A-16	Sequence 16, Appl1
5	605.2	20.8	3128	US-08-716-449-1	Sequence 1, Appl1
6	587.8	20.2	2909	US-08-104-158-1	Sequence 1, Appl1
7	369	12.7	11478	US-08-981-803-29	Sequence 29, Appl1
8	68.4	2.3	2426	US-08-528-026C-3	Sequence 3, Appl1
9	68.4	2.3	7218	US-08-232-463-14	Sequence 14, Appl1
10	43.2	1.5	1404	US-08-204-656B-1	Sequence 1, Appl1
11	41.4	1.4	1404	US-08-204-656B-3	Sequence 3, Appl1
12	41.4	1.4	1404	US-08-204-656B-7	Sequence 7, Appl1
13	41.4	1.4	1404	US-08-470-702-1	Sequence 1, Appl1
14	41.4	1.4	1404	US-08-470-702-2	Sequence 2, Appl1
15	41.4	1.4	1404	US-08-470-702-4	Sequence 4, Appl1
16	41.4	1.4	1404	US-08-467-831-1	Sequence 1, Appl1
17	41.4	1.4	1404	US-08-467-831-2	Sequence 2, Appl1
18	41.4	1.4	1404	US-08-467-831-4	Sequence 4, Appl1
19	41.4	1.4	661	US-08-961-083-77	Sequence 77, Appl1
20	40.2	1.4	1404	US-08-204-656B-5	Sequence 5, Appl1
21	39.8	1.4	1404	US-08-470-702-3	Sequence 3, Appl1
22	39.8	1.4	1404	US-08-276-452A-25	Sequence 25, Appl1
23	39.8	1.4	1430	US-08-798-744-25	Sequence 25, Appl1
24	37.8	1.3	1430	US-08-276-452A-24	Sequence 24, Appl1
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28	37	1.3	2100	US-07-927-316A-1	Sequence 1, Appl1
29	35	1.2	198	PCT-US95-10668-1	Sequence 1, Appl1
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31	35	1.2	7101	US-08-480-604A-9	Sequence 9, Appl1
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34	34.6	1.2	1376	US-08-722-184-3	Sequence 3, Appl1
35	34.6	1.2	1376	US-09-043-937A-7	Sequence 7, Appl1
36	34.6	1.2	5893	US-08-592-126-54	Sequence 54, Appl1
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ALIGNMENTS

RESULT 1
US-09-087-277-1
; Sequence 1, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087, 277B
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
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; NAME/KEY: CDS
; LOCATION: (189)..(2825)
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; LOCATION: (92)..(2156)
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; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
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; FEATURE:

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OTHER INFORMATION: or Phe.
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US-09-087-277-1

Query Match 47.5%; Score 1382.4; DB 4; Length 3074;
Best Local Similarity 76.6%; Pred. No. 0;
Matches 1689; Conservative 0; Mismatches 515; Indels 0; Gaps 0;

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RESULT

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US-08-941-445A-14

Sequence 14, Application US/08941445A

Patent No. 6107060

GENERAL INFORMATION:

APPLICANT: Keeling, Peter

APPLICANT: Guan, Hanping

TITLE OF INVENTION: Starch Encapsulation

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Greenlee, Winner and Sullivan, P. C.

STREET: 5370 Manhattan Circle

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/941.445A

FILING DATE: 30-SEP-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/026,855

FILING DATE: 30-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Winner, Ellen P

REGISTRATION NUMBER: 28,547

REFERENCE/DOCKET NUMBER: 89-97

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 2725 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: not relevant

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Zea mays

FEATURE:

NAME/KEY: sig_peptide

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; LOCATION: 91..264
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 265..2487
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..2490
US-08-941-445A-14

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Query Match 43.0%; Score 1251.8; DB 3; Length 2725;
Best Local Similarity 75.4%; Pred. No. 0;
Matches 1556; Conservative 0; Mismatches 507; Indels 0; Gaps 0;

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US-08-941-445A-16

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Db	479	AACAGGGAAGATGCTGGCATAGCTATCTGTGAATGGCTCTGCTGCTCAGGAACGAA	538
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Db	539	GTTATTGGGGAATTCATATGATGGAACGGTCTTAAACCATGATGGAAGAACCACTTT	598
QY	720	ggtctctggagatccttttgcgcgaataigcagatggttccacccaatttcccatggt	779
Db	599	GGGTGTTGGAGATTTAAGATTCC---TGAATGTGACATAGACCAAGTCATTTCACACAC	655
QY	780	tctcgaaataagatacgy---cagtataactcatctctgccaacaaagtattatccgct	836
Db	656	TCCAGAGTTAAAGTTTCGTTTCAAACTGTAATGAGAGTGGTGAATGATGATGCCGTGT	715
QY	837	tggatcaaatctctcagttcaag-----caccaggtgaactcccatataatgagatcac	890
Db	716	TGGATTAATATAGCCACATGCAACGCCCAAAAGTTTGAGAGCACCATTGATGGTGCTAC	775
QY	891	tatgataccctcccgagagagagagatggtgttcaaaatctctcgaacgaagagacaaa	950
Db	776	TGGGACCCACACCTTCGAAAGAGTACACTTCAAAATACCTGCCCCCTCCCAACCCCGA	835
QY	951	taacttcggaattatgagtcgcagcttggaaatgagtagtagcagagccagatataacaa	101
Db	836	GCCCCACGATCTACGAAGCACATGTCGGATGAGCAGACTCTGAGCCACGTAAATTCG	895
QY	1011	tatgcacaatttagagatgagtgtctctgcgcataaagaacgtctgctcacaatgctgt	107
Db	896	TATCGTGATTTGGCAGATGATGTTTTTACTCTGGATTAAAGCAATAATCTAATTAATCTGTC	955
QY	1071	caagtcataggtctatcaagaagcatcatabathatgctagtttggatcaagtcacaaac	1133
Db	956	CAGTTGATGCGCATATGGAACATCTTACTATGATCATCTTGGATATCTGTTTACAAAC	1011
QY	1131	ttttagtcagctcagaagcagatttggaaacctctabatttaagttcctcaagataaa	1199
Db	1016	TTTTTTGCTGTGAGCAATAGATATGGAACCCGAGGACCTTAAGATTCGTAGATGAATA	1077
QY	1191	gctcaagagtttagtctctctgtctcatgataatgttctatagacagatcaataaat	1251
Db	1076	GCACATACCTTGGGTTTACAGAGTCTGTGGATGTAGTTCACAGTACGACAACTAAT	1133
QY	1251	agcttgagtggtcgcgaatatgtttgat-----gatacgatggtcaactacttcaac	1307
Db	1136	GTCACATGATGCGCTCAAGAGCTGTGAATTTGGCCAAAGGTTCTCAAAATCTACTTCAAT	1199
QY	1302	tctagacaacaggggtcatalcatcatctgtagtctggaactctgcctttcaacatggaagctg	1361
Db	1196	GCTGAGAGCGAGGGTACCAATATGTTGGGATATGCAAGGCTGTTCAACTATGCCAAATTG	1255
QY	1362	gaggttctcaaggtctctctcttccaatctgcaaggttggtgtgttgaatgatacaagttgat	1421
Db	1256	GAGGTTTTCGTTTCCTTCTTCCAACTTAGGTTGGGCTGTAAAGATTAACCTTTGAC	1315
QY	1422	gggttcaaatctttagtggggagaaactcaatgataccatcatatgatttgcagttgat	1481
Db	1316	GGATTTGCATTTGATGGAATTAATCTTCTATCTGTATGTTTCATCATATGGAATTAATGGA	1377
QY	1482	tttacgcgaactacaatlgaaatacttggatlgaaatgaaactgtagttagtctgtgttat	1541
Db	1376	TTTACAGGAACCTTAATATGATATTTTCAGGAGGCTTACAGATGTGATCTGTGGCTAT	1435
QY	1542	ttagatgcgtttagatgataatgataagctctctcccaagagtcgttgcacatttggtaa	1601
Db	1436	TTAATGTTGGCAATTAATCTGATTTACACAGATTTTCCACAGCGCAACTGTATTATCCGAA	1495
QY	1602	gagtgtagtggaaatgccaaagtttgcattccggttggaaatgagtggtgtgttgcttat	1661
Db	1496	GATGTTTCTGTATGCCGGGCGCTTACCGGCGCTGTTTTCAGAGGAGAAATTGCTTTGAT	1555

QY	1662	taaggtctcaacatggccgtgtgctgataaabaaggcttggatattacag--aaagaagat	1718
Dp	1556	TACCGCTGGCAATGGCAATCCGACGTAGTGTGATAGATTATTAAAGAAATAAAGAT	1615
QY	1719	gaagatctggaataatgggtgacattgacatacgtcgcacaacaagcgggtgtgtggaaga	1778
Dp	1616	GAGATTTGGCCATGAAAGAGAAACATCATGATCTTTGACAAATAGACATATATACAGAAAG	1675
QY	1779	tgtgttcttaagctgaaagatatacgaacgaagcccttgtttgtggaacaaactatgcaatt	1838
Dp	1676	TGTATAGCATATTCGAGAGCCATGATCATGTATTTGTCGGGACAAACCATTTGCAATT	1735
QY	1839	tggcgataggaacaagatatgtatgacctacggcctctggaacgaacacacacccctcc	1898
Dp	1736	CTCCCTAATGACAAAGATGATTTCTCGCATGCTCTGCTTACAGATGCTTCTCTGTT	1795
QY	1899	atgatactgtgagtagcatctgacacaacatgcatcagaactatcacatggaattgagcga	1958
Dp	1796	GTTGATCGAGAAATTCGCGCTTCACAGATGATCCATTTTTCACAAATGCGCTTGGAGGA	1855
QY	1959	gaaggaatttgatatttttgggaataatgtatgacaccccgatggatgtatttcca	2018
Dp	1856	GAGGGTACCTCATTTTCATGGGTACGAGTTGGCCATCTCGATGGATGTACCTTCCT	1915
QY	2019	aagaggtgatacatctctccacgtgtgtaattgttccctgggaacaatlaacgtatgat	2078
Dp	1916	AGAGAG-----GGCAATATATTTGAGGTTATGAC	1942
QY	2079	aaatggcgggtgtgtgttgaatctaggaacaattcaaacgactctgaagatacaatgaagaa	2138
Dp	1943	AAATGTTAGACCCAGTCGAGACCTCGCAGATAGGGAACATTGAGATACAGTTTATGAAT	2002
QY	2139	gaatttatcaagaacattgcgcctcttggaaagacctatggtttatgaactctgaagac	2198
Dp	2003	GCAATTTATAGACTATGAAATTTGGCTCGATGAAAAATCTCTCATTCCTCGCATCAGAAAA	2066
QY	2199	caatacaatacgaagaaaggttgaagaagatcgaatactgtgtcttgcgaaggggaaacct	2256
Dp	2063	CAGATAGTAAACAGACATGATGATGATTAATAAAGTTGTTGTTGTAAGCTGTGACCTG	2122
QY	2259	gtttttgtatcaattttcatatttgagctagaagatctggatlaacgaattgctgcgta	2318
Dp	2123	GTAATTTGATTAACATCTTCCACCCAAATACACATACGAAGGATATAAATTGGATGTGAC	2183
QY	2319	aagccgaagaaatgacaagaatagctcttgatctcgaatcgaatcccttgttttggagcttgg	2376
Dp	2183	TTTGCAAGGAAATACAGAGTTGCACTGTGGCAGTGAATCTTTGGGAATTTGCTGGCCATGSA	2244
QY	2379	aggcttagtcaatgatacgaagcaactta	2406
Dp	2243	AGAGCTGGCTCATGATGTTGACCATTTTGA	2270

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Page 10

OY	1030	atggctctctgcatacaaaaagctcgtgctacagctcgttcacgtccatctcaag	1089
OY	5362	atgttttaacctggtatgaagcaataactatatactatcgttcagttggtgcata	5421
OY	1090	agcaatcatattatgcagatttttggtgatacagtcacaaactttatgcac	1149
OY	5422	aacctcttactatcagatcatttttggtatatacgttacaactcttttgc	5481
OY	1150	gatttggaacctctgatagtattaaagctcttaataagataaagctaa	1209
OY	5482	gattctggnaaacccggagagaccataaagatcgtgtatataaagcaaat	5541
OY	1210	tgtctctcaatgatattgtttcatagcaatgatacaactaatacgtttg	1269
OY	5542	aggtctctggtgagtgtatgattccagatcattgcaagcaataatgata	5601
OY	1270	tgattgag-----gtaacgagatgatactacttcaactctgagac	1320
OY	5602	gattgataatggccaaggtctccaaagaaactctacttcaatctgagag	5661
OY	1321	attgagatggaactccgcgcttccaactatgagggccggagagttc	1380
OY	5662	ataagttggtgataagcaagcgtgttccaactatgcgaattggagag	5721
OY	1381	tttcaaatcaaaagttggtttgtgataatgacaagtttatggttccaa	1440

Db	5722	tttccaaatttgagtggtggtgcgtgaagaagatataaactttgaacggaatttgattgattgtagaa	5761
Qy	1441	tgcattcaatgatattacacccatgatgattggaagtgaaattatccacggcacaactacatg	1500
Db	5782	taactcttcacgtctatgatttcatacatgatgaatcaataatgatgatttacaggaactaata	5841
Qy	1501	aactcttggtatagcaactgatattgaattctgtgattatattgaagtcggttgtaagtga	1560
Db	5842	agtattcttcagcagagctcctcagaatgattgtagctgtgctcatcttaaacgttgcacataac	5901
Qy	1561	tgattcatcgtgctcctctccacagagctgcacccattgtaagaagtgttagtggaatgcaca	1620
Db	5902	tgattcacacaagaattttccccaagtcgaactgttatctccgaagatgctctgttatgcg	5961
Qy	1621	cagtttgcatcccggtctgaagaatggtggtgttggtcttgattatgctgtccaaatggcgtc	1680
Db	5962	gacctggcgcgcgcgcttctctcgaagggaagaaattggtgtttgttccgcgcgcgaatggaca	6021
Qy	1681	ttgtcgtgataaatggtgtgagaattattcaag---aagagagataagaatttgaaatatgggtc	1739
Db	6022	tcccgagatagaaggatagaatattatcttaagaagaataagatgctgaaagattggtccatgaag	6081
Qy	1738	acattgtacatatgctgcacacaacagcggtggtgttggaagaagtgtgtttttttgtcgtgaa	1797
Db	6082	aagtaacaacaggttttgacaataagagaatatacacagaagaatgtaacagcatatgtcggaaga	6144
Qy	1798	gtcatgtaccagcgccct	1814
Db	6142	cccatgtatcaggtatct	6158

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: RESULT 8
: US-08-983-440-29
: Sequence 29, Application US/08983440
: Patent No. 6232122
:
: GENERAL INFORMATION:
: APPLICANT: POUJSEN, Peter
: TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
: FILE REFERENCE: 674509-2003
: CURRENT APPLICATION NUMBER: US/08/983,440
: CURRENT FILING DATE: 1998-04-17
: EARLIER APPLICATION NUMBER: 9514437.4
: EARLIER FILING DATE: 1995-07-14
: EARLIER APPLICATION NUMBER: PCT/EP96/03053
: EARLIER FILING DATE: 1996-07-12
: NUMBER OF SEQ ID NOS: 35

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1 SOFTWARE: PatentIn Ver. 2.0
2
3 SEQ ID NO 29
4 LENGTH: 11478
5
6 TYPE: DNA
7
8 ORGANISM: Solanum tuberosum
9
10 FEATURE:
11 NAME/KEY: variation
12 LOCATION: (1)..(11478)
13 OTHER INFORMATION: B stands for G or C or T/U
14
15 FEATURE:
16 NAME/KEY: variation
17 LOCATION: (1)..(11478)
18 OTHER INFORMATION: R stands for G or A
19
20 FEATURE:
21 NAME/KEY: variation
22 LOCATION: (1)..(11478)
23 OTHER INFORMATION: K stands for G or T/U
24
25 FEATURE:
26 NAME/KEY: variation
27 LOCATION: (1)..(11478)
28 OTHER INFORMATION: W stands for A or T/U
29
30 FEATURE:
31 NAME/KEY: variation
32 LOCATION: (1)..(11478)
33 OTHER INFORMATION: M stands for A or C
34
35 US-08-983-440-29

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	Query Match:	12.7%;	Score 369;	DB 4;	Length 11478;
	Best Local Similarity	64.3%;	Pred. No. 8.5e-103;		
	Matches	590;	Conservative	0;	Mismatches 315; Indels 12; Gaps 2
QY	910	agaagtatgtgttcaaaaatccctcagcgcaaaagagacaaatccatctcggtattatgct	969		
DB	5242	acaagttaccacttcaaatatccctccgcctccccaaccccgagccccaagtatcagaag	5301		
QY	970	cgcagctgtgaatgagtagtaagcagagccagtaattacaacatctgcacacttctgagatg	1029		
DB	5302	cacacgtctgcatatgagacatctcgagccagcagtaattctgatatctgtatgttcagatg	5361		
QY	1030	atgtctccctccgcgatcaaaaaagcttgcgtacaaatgctgtttcagctcatgtcttcaag	1089		
DB	5362	atgttttccctccgcgatlaaagcgaataactataatactgttccagttctgtcccttaatg	5421		
QY	1090	agcattcatatacgcacagttctgggtatcacgtccacaactttatgcagctc;gagcc	1149		
DB	5422	aacacttctactatcgtacatttggatatatctgttacaacttttctgttgcgcagta	5481		
QY	1150	gattttggaaccccgatgatattaagctctaaataataaagctcaagatgaagcttc	1209		
DB	5482	gatatggaaaccggagagacctaaagtatctgtatagataaagacatatagcttgttttac	5541		
QY	1210	tgtgtctcatagatattgttcatagacatcgtacaaactaatagctttgatgtggtc;tgaaata	1269		
DB	5542	aggtcttcggtggagtgatgttcacagttcagacgaataatctaacatgtatgctc;ttcaatg	5601		
QY	1270	tgattgat-----gtacaggaatgctactactttcaactcttggaacagcggtgtatc	1320		
DB	5602	gcttttgatattggccaagagttctccaagaatccacttcttcaatctgtggagagcgatgtaac	5661		
QY	1321	attgtaattgtggactctgcgcttttcaactatgagagcgctggaggtcttaaggtcttcctc	1380		
DB	5662	ataaagtcttggaatagacagcgctgttcaactatgcgaatctggagaggtctctgtctccctc	5721		
QY	1381	tttcaaatgcaagagtggtgtgttgatgatacagaagttctatgtgtctcagattatgaggg	1440		
DB	5722	tttccaacttgagtggtgtgtgtagaagaatataactttgacggaattctgattttatgaa	5781		
QY	1441	taacttcaatatgataaacccatataatgatttgaggtagattttacagcaac;acaatg	1500		
DB	5782	taacttcatagctgtatgttcatcatcagaatcaatgagatttacaagaaac;ataatg	5841		
QY	1501	aatactttgataatgcaacagatgataagctgtgtttattttgagtgcgttgtaatgata	1560		

Db	5842	agatattcagcggcgctacagatggttgatgcgtgtgtctatttaagtgtggccaataatc	5901
Qy	1561	tgatatacgtctctctcccaagagcgtcacatcgtgtgaagaatgtatagtggaatgccaa	1620
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Qy	1621	cagtttcgcttcgcggttgaaagatggtgtgtgtgccttgattatcgtctccaaatgctgt	1680
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Qy	1681	ttgtcgtataaattggtgtgagattattccag---aagagagatgaagatttggaaatgggtgt	1737
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Qy	1738	acattgtacatatcgtgcacacaagcgtgtgttgaaagtgtgttcttatcgtctgaa	1797
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Db	6142	cccatgtatcaggtattt	6158

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RESULT 9
US-08-528-026C-3
: Sequence 3, Application US/08528026C
: Patent No. 6248566
: GENERAL INFORMATION:
: APPLICANT: IMANAKA, Tadayuki
: APPLICANT: TERADA, Yoshinobu
: APPLICANT: TAKAHARA, Takeshi
: APPLICANT: YANASE, Michio
: APPLICANT: OKADA, Shigetaka
: APPLICANT: TAKATA, Hiroki
: APPLICANT: NAKAMURA, Hiroyasu
: APPLICANT: FUJII, Kazutoshi
: TITLE OF INVENTION: GLUCAN HAVING CYCLIC STRUCTURE AND METHOD FOR PRODUCING THE SAME
: FILE REFERENCE: 9900-0002..20
: CURRENT APPLICATION NUMBER: US/08/528,026C
: CURRENT FILING DATE: 1995-09-13
: PRIOR APPLICATION NUMBER: US 08/415,152
: PRIOR FILING DATE: 1995-03-31
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Bacillus stearothermophilus (Strain TBRE14)
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (385)..(392)
: OTHER INFORMATION: S SD sequence
: NAME/KEY: misc.feature
: LOCATION: (402)..(2357)
: OTHER INFORMATION: P CDS
: US-08-528-026C-3

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Query Match	2.3%;	Score 68.4;	DB 4;	Length 2426;
Best Local Similarity	48.5%;	Pred. No. 8.3e-11;		
Matches 220;	Conservative	0;	Mismatches 231;	Indels 3;
				Gaps 1;

QY	1003	ttacacatattagccaacttttagagatgagttgcttctcgcatacctaaagaagctgtgcata	1065
Db	895	tttaacacgtaccgtagaagatgagccgatacgtacctcgatgtgtcctgcatactgttgltta	954
QY	1063	atgctgttcagcgtcatatgctcatltaaaagatcatcatatattctagttttggatcacg	1122
Db	955	cgcacattgagttgcttctctctcgtcgagatcatcgcttcgacgcgtcgtggggtcatcaag	1014
QY	1123	tcacaaactttatgcagctagcagccgcgatttggaaactcctgatgtttaaagctctctaa	1188

Db	1015	gaacagggtatlaatgcgtaacagatgcgtatcgtatggtatgcgcacaacagacttcaatgcttcgc	1074
Oy	1183	tagataagctcaacagagtttagtctctctcttccatcgatattttcttaacatgatcat	1242
Db	1075	tcgacgcgttcacatcagcgcggaatcgggtacattatgtaacgcggtgtccggggacatttt	1134
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Db	1145	gcaaggagagc---ccatagggtatataatgttttatatgcccgcacgtatgatatacgca	1190
Oy	1303	cttgaccacgcggggtcatctatgtaatgtagggaactccgccttccaactatgtagagctgg	1362
Db	1132	atgaaaagacccggaaatatacgtttcgtggggagcgcacatttgatttaaggcaacccgg	1251
Oy	1363	aggtctaaagttctctctcttccaatgcaagtggtgtgtgtaatgagatacaagttttgat	1422
Db	1252	aagtcgcaagtttctcattcgaatcgaacgcattggttcgctcagattaccatactacgag	1311
Oy	1423	ggttcagaattgtagtggtgtaactcaatgatga	1456
Db	1312	ggttcgcggtcgaatgcggttgccaatatgtttta	1345

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US-08-232-463-14/c
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFFELINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 24472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTgpt-F15

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; INFORMATION FOR SEQ ID NO: 14
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 718 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
; IMMEDIATE SOURCE:
;     CLONE: pTgpt-Fls
;
US-08-232-463-14

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REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-470-702-1

Query Match 1.4%; Score 41.4; DB 1; Length 1404;
Best Local Similarity 56.1%; Pred. No. 0.012; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 61;
QY 1100 ttatgctagtttgggtatcagtcacaaactttatgcagctagcagccgatttgaac 1159
DB 231 ttatgcttattcattggttctgagtgagaaacattatgacaaatgaaactttggtac 290
QY 1160 tccctgatgatttaagctctctaataagataagctcagagttagctcttcttctcat 1219
DB 291 tgcgatgatttgaagctcttggcacaagaattgacagatcgatgattgttattggt 350
QY 1220 ggaattgttcataagccat 1238
DB 351 ggatattcgttaccacacat 369

RESULT 15

US-08-470-702-2
Sequence 2, Application US/08470702
Patent No. 5631149

GENERAL INFORMATION:

APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 810 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-470-702-2

Query Match 1.4%; Score 41.4; DB 1; Length 1404;
Best Local Similarity 56.1%; Pred. No. 0.012; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 61;
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Fri Aug 10 16:32:41 2001

us-09-297-703a-28.Aug9.rni

Page 15

The first part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the business to have a clear and concise record of all income and expenses. This will help in the preparation of the tax return and in the event of an audit.

The second part of the paper discusses the importance of keeping the books up to date. It is important to record all transactions as they occur, rather than waiting until the end of the year. This will help in the preparation of the tax return and in the event of an audit.

The third part of the paper discusses the importance of having a good system of internal controls. This will help in the prevention of errors and in the detection of fraud. It is important to have a system of checks and balances in place.

The fourth part of the paper discusses the importance of having a good understanding of the tax laws. It is important to know the rules and regulations that apply to the business. This will help in the preparation of the tax return and in the event of an audit.

The fifth part of the paper discusses the importance of having a good understanding of the accounting principles. It is important to know the rules and regulations that apply to the accounting. This will help in the preparation of the tax return and in the event of an audit.

The sixth part of the paper discusses the importance of having a good understanding of the business. It is important to know the nature of the business and the needs of the customers. This will help in the preparation of the tax return and in the event of an audit.

The seventh part of the paper discusses the importance of having a good understanding of the market. It is important to know the current market conditions and the future prospects of the business. This will help in the preparation of the tax return and in the event of an audit.

The eighth part of the paper discusses the importance of having a good understanding of the competition. It is important to know the strengths and weaknesses of the competitors. This will help in the preparation of the tax return and in the event of an audit.

The ninth part of the paper discusses the importance of having a good understanding of the industry. It is important to know the trends and developments in the industry. This will help in the preparation of the tax return and in the event of an audit.

The tenth part of the paper discusses the importance of having a good understanding of the economy. It is important to know the current economic conditions and the future prospects of the economy. This will help in the preparation of the tax return and in the event of an audit.

GenCore version 4.5
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		Burton, R.A., Bewley, T.D., Smith, A.M., Bhattacharya, M.K., Tatge, H.,										
		Ring, S., Bull, V., Hamilton, W.D. and Martin, C.										
		Starch branching enzymes belonging to distinct enzyme families are										
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		Plant J. 7 (1), 3-15 (1995)										
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		Burton, R.A.										
		Direct Submission										
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolus. (Bases 1 to 3360)
 TITLE Nozaki, K., Ito, H., Matsui, H. and Honma, M.
 JOURNAL Phaseolus vulgaris L. mRNA for starch branching enzyme 1
 REFERENCE Published only in Database (1999) In press
 AUTHORS 2 (bases 1 to 3360)
 TITLE Nozaki, K., Ito, H., Matsui, H. and Honma, M.
 JOURNAL Direct Submission
 Submitted (03-JUL-1999) to the DDBJ/EMBL/GenBank databases.
 Hirokazu Matsui, Hokkaido University, Faculty of Agriculture,
 Kita-Ku, Kita 9 Nishi 9, Sapporo, Hokkaido 060-8589, Japan
 (E-mail: mhiro@chem.agr.hokudai.ac.jp, Tel: 81-11-706-2500,
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 REFERENCE 1 (sites)
 AUTHORS Abe, J. and Oriuchi, T.
 TITLE Starch-branching enzyme cDNA from sweet potato (Ipomoea batatas)
 JOURNAL Published only in Database (2001) In press
 REFERENCE 2 (bases 1 to 2517)
 AUTHORS Abe, J. and Oriuchi, T.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAY-2000) Jun-ichi Abe, Kagoshima University, Faculty

of Agriculture; Koriimoto 1-21-24, Kagoshima, Kagoshima 890-0065,
 Japan (E-mail: j.abechem.agri.kagoshima-u.ac.jp,
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 AUTHORS Fisher,D.K., Gao,M., Kim,K.N., Boyer,C.D. and Guiltinan,M.J.
 TITLE Two closely related cDNAs encoding starch branching enzyme from
 Arabidopsis thaliana
 JOURNAL Plant Mol. Biol. 30 (1), 97-108 (1996)
 MEDLINE 96197401
 REFERENCE 2 (bases 1 to 2542)
 AUTHORS Fisher,D.K., Gao,M., Kim,K.N., Boyer,C.D. and Guiltinan,M.J.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-1995) Dane K. Fisher, Horticulture, Pennsylvania
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VERSION	AF000004.1	GI:2764395		
KEYWORDS	Sbe-II gene; starch branching enzyme II.			
SOURCE	Potato.			
ORGANISM	Solanum tuberosum			

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 2493)
Larsson/C.T.A.
Direct Submission
Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell

REFERENCE 2 (bases 1 to 2493)
AUTHORS Larsson, C.T., Khoshmoodi, J., Ek, B., Rask, L. and Larsson, H.
TITLE Molecular cloning and characterization of starch-branching enzyme II from potato
JOURNAL Plant Mol. Biol. 37 (3), 505-511 (1998)
MEDLINE 96278379

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gene

CDS

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BASE COUNT
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Db 285 TGGTAAACTCGAGAGCTTAATAACATTAAATACTTCTGAGAAGACAATTATTTGATGAATC 344

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ACCESSION A58169
VERSION A58169.1 GI:3713894
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2578)
AUTHORS Cooke, D., Debec, M., Gidley, M.J., Jobling, S.A., Safford, R.,
SIDEBOTTOM, Christopher, M. and Westcott, R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
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Db	2156	GGACAAACGATATGATGATTTTATGTGCTTTGGATACCCGTCAAACATTAATATGATGCT	2215
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REFERENCE	1 (bases 1 to 2576)	
AUTHORS	Cooke,D., Debel,M., Gidley,M.J., Jobling,S.A., Safford,R.,	
TITLE	Siddebottom, Christopher M. and Westcott,R.J.	
JOURNAL	IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION	
COMMENT	Patient: WO 9634986-A 16 07-NOV-1996;	
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 REFERENCE 1 (bases 1 to 2992)
 Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M., Debel, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
 A minor form of starch branching enzyme in potato (Solanum tuberosum L.) tubers has a major effect on starch structure; cloning and characterisation of multiple forms of SBE II
 unpublished
 2 (bases 1 to 2992)
 Jobling, S.A.
 Direct Submission
 Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK

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JOURNAL
Plant Mol. Biol. 30 (1), 97-108 (1996)
MEDLINE
96197401
REFERENCE
2 (bases 1 to 2542)
AUTHORS
Fisher D.K., Gao M., Kim K.-N., Boyce C.D. and Gollub A.L.

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AUTHORS	Larsson, C.T.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell Research, Genetic Center, Swedish University of Agricultural Sciences, Box 7055, S-750 07 Uppsala, SWEDEN		
REFERENCE	Larsson, C.T., Khoshnoodi, J., Ek, B., Rask, L. and Larsson, H.		
AUTHORS	Molecular cloning and characterization of starch-branching enzyme II from potato		
TITLE	Plant Mol. Biol. 37 (3), 505-511 (1998)		
JOURNAL	98278379		
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